

FIGURE 1

Find Neighbors
and Assemble
Flow Diagram

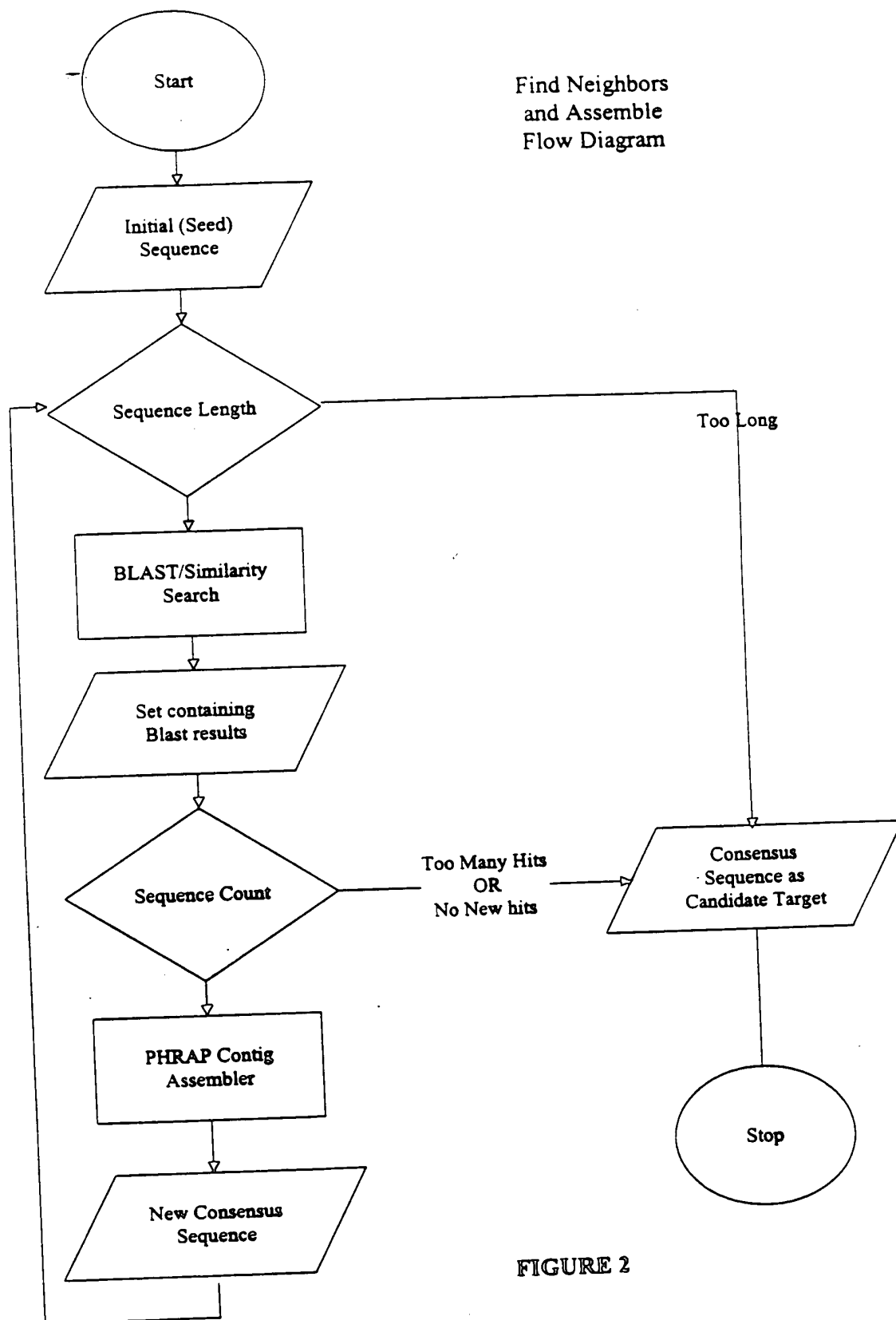


FIGURE 2

-BlastParse

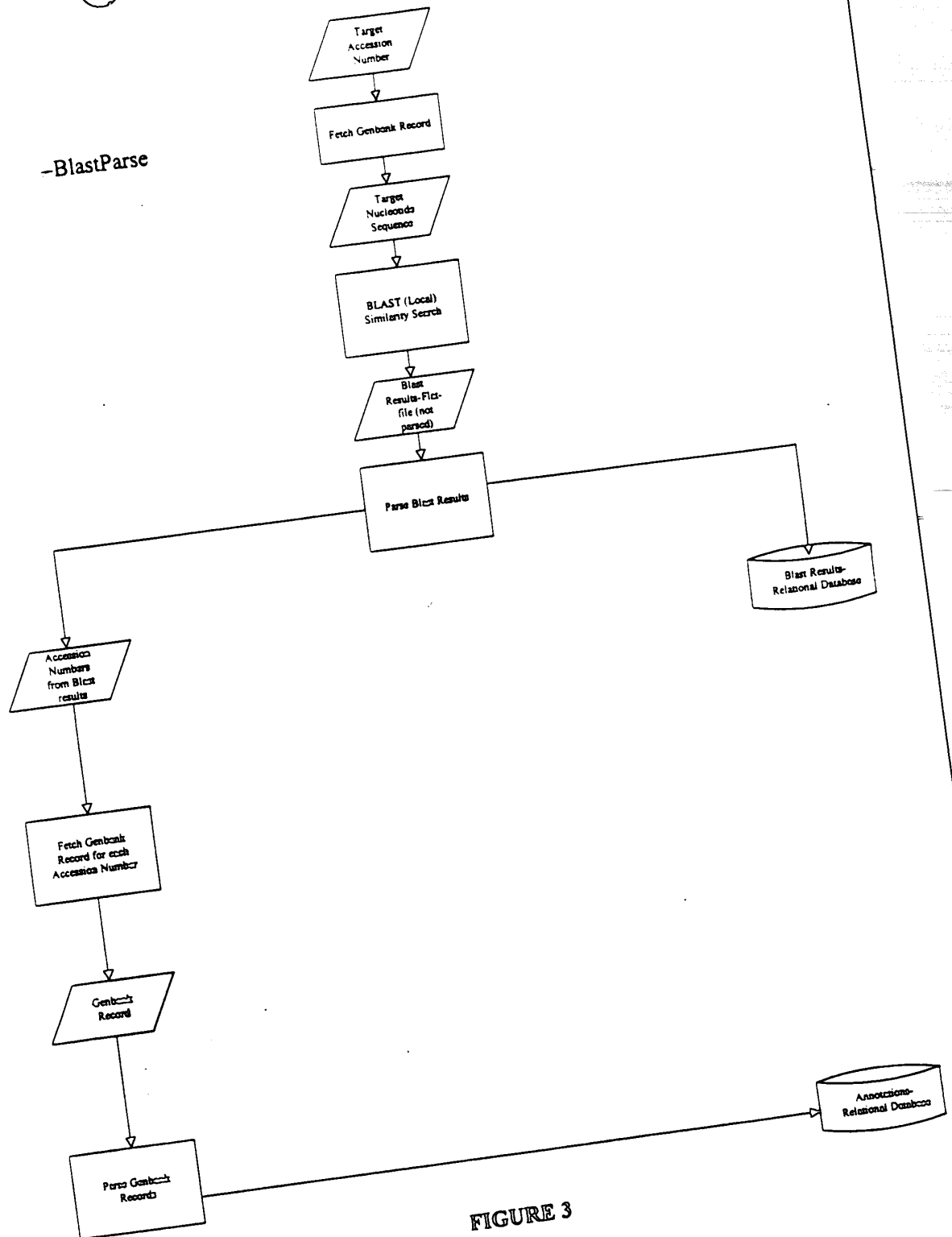


FIGURE 3

Q-Compare

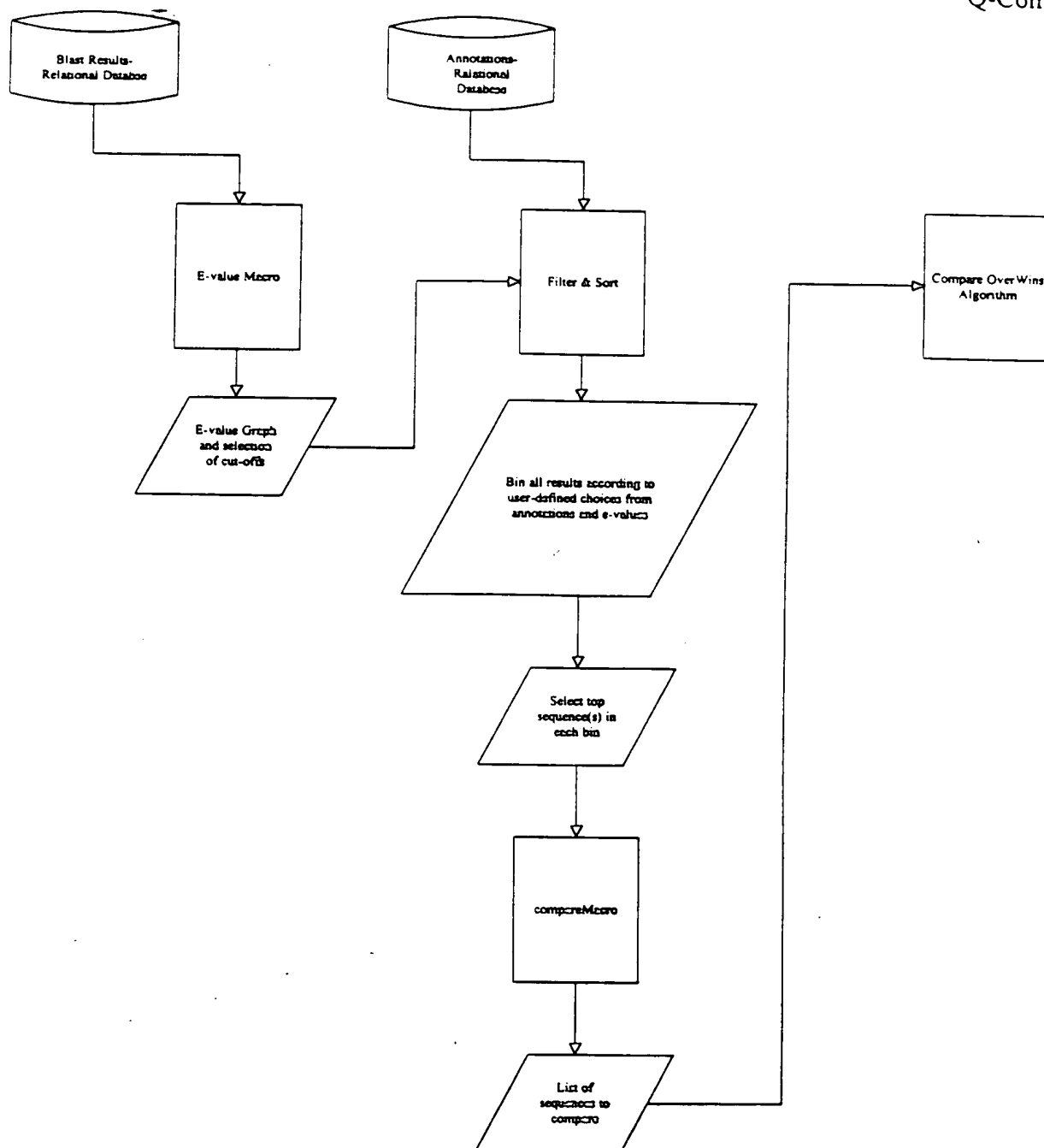


FIGURE 4

CompareOverWins Algorithm Flow Chart

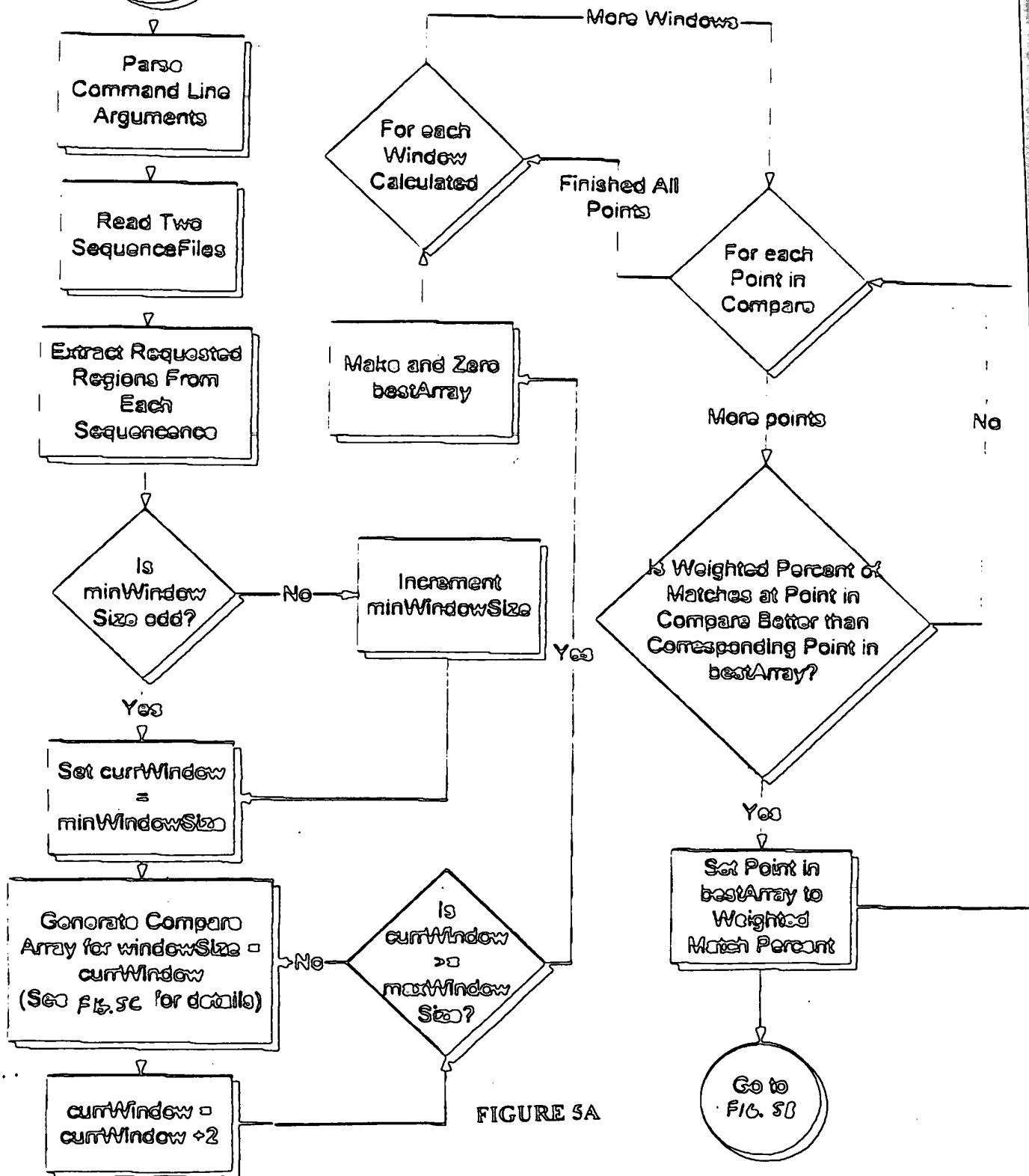


FIGURE 5A

CompareOverWins Algorithm Flow Chart

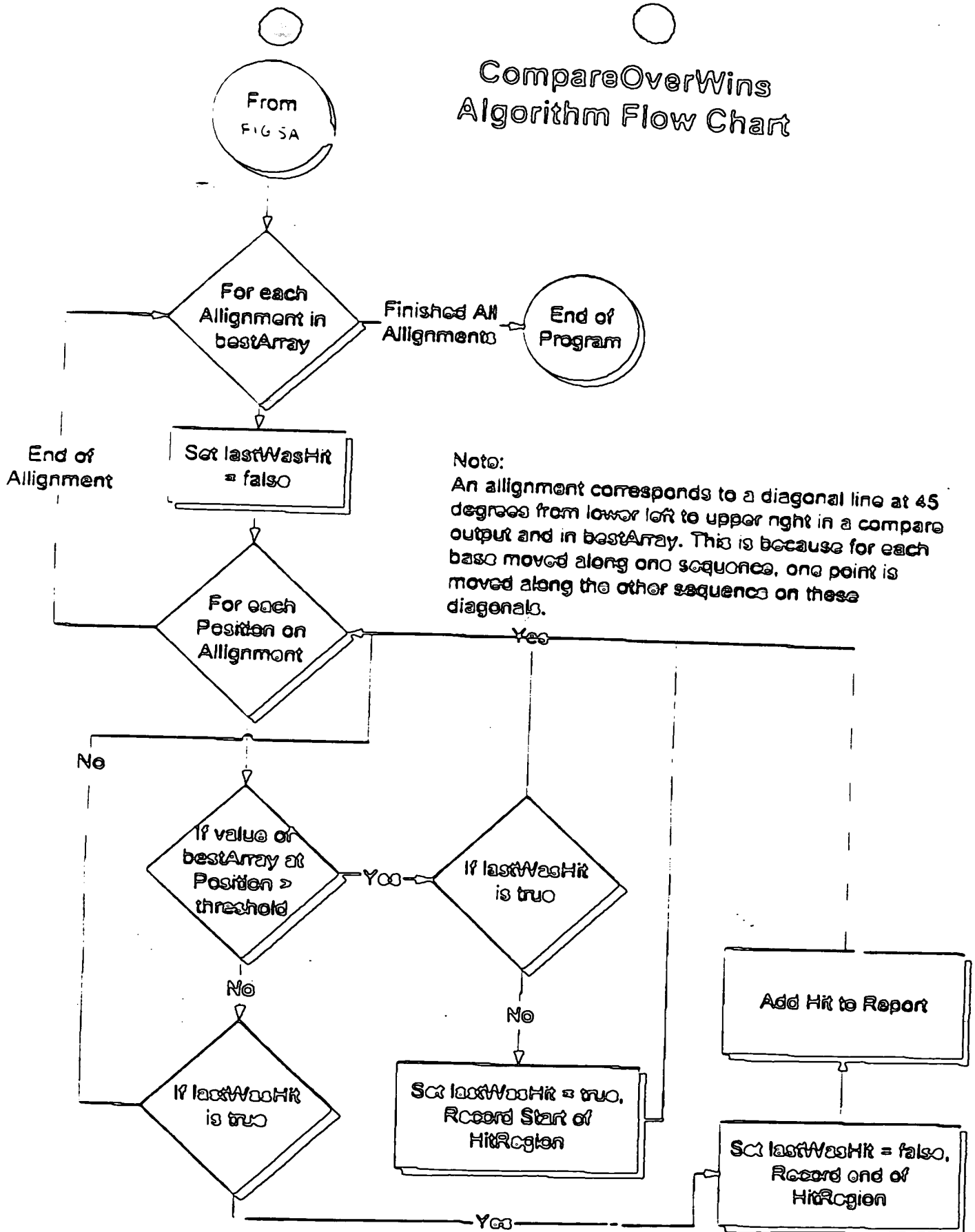


FIGURE 5B

CompareOverWins Algorithm Flow Chart Basic Compare

Input:
Sequence A length a
Sequence B length b
Window Size

Output:
Array of size a by b of unsigned chars (0-255)
Each point represents the number of matches in the window at that alignment and position

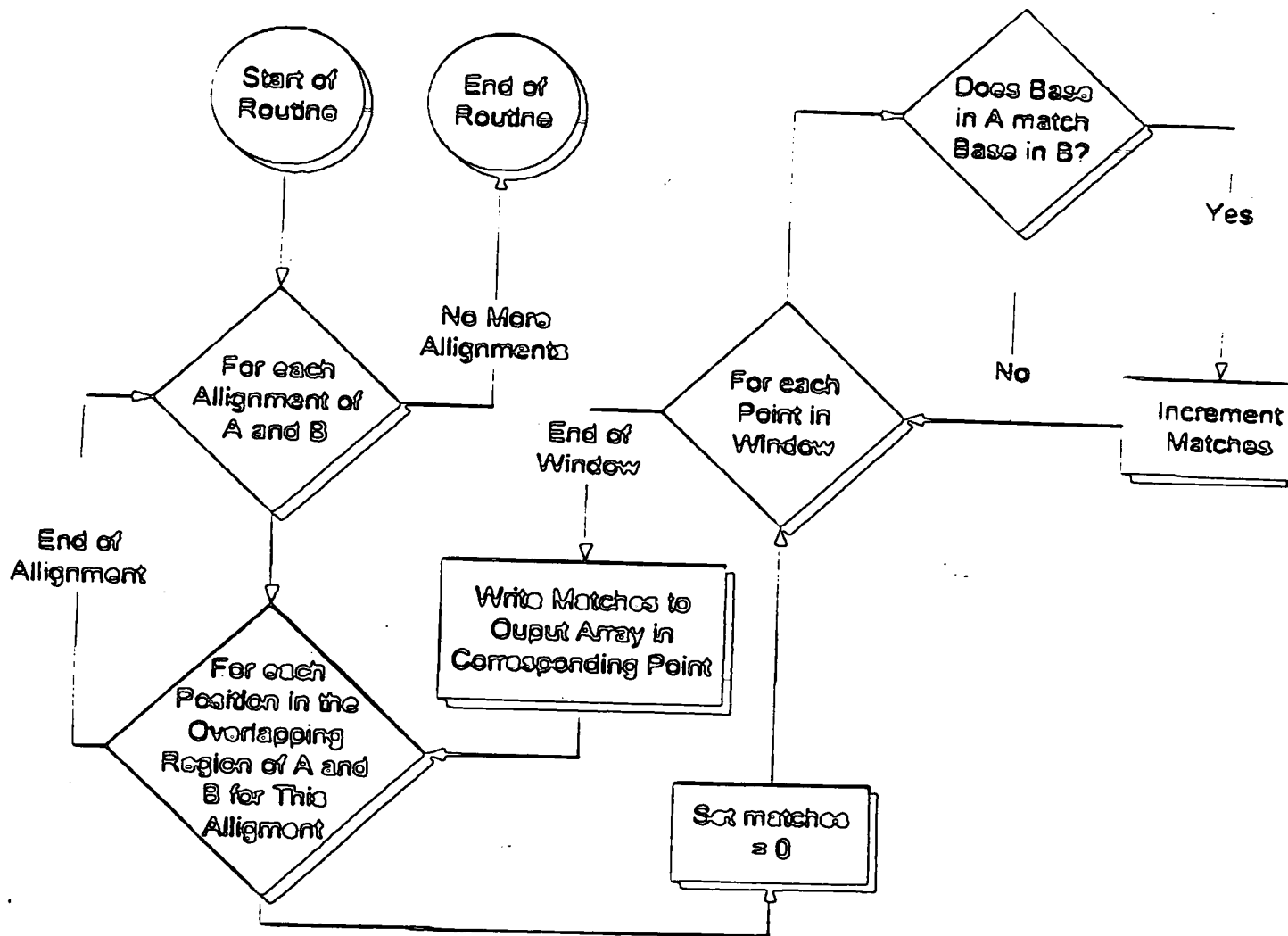
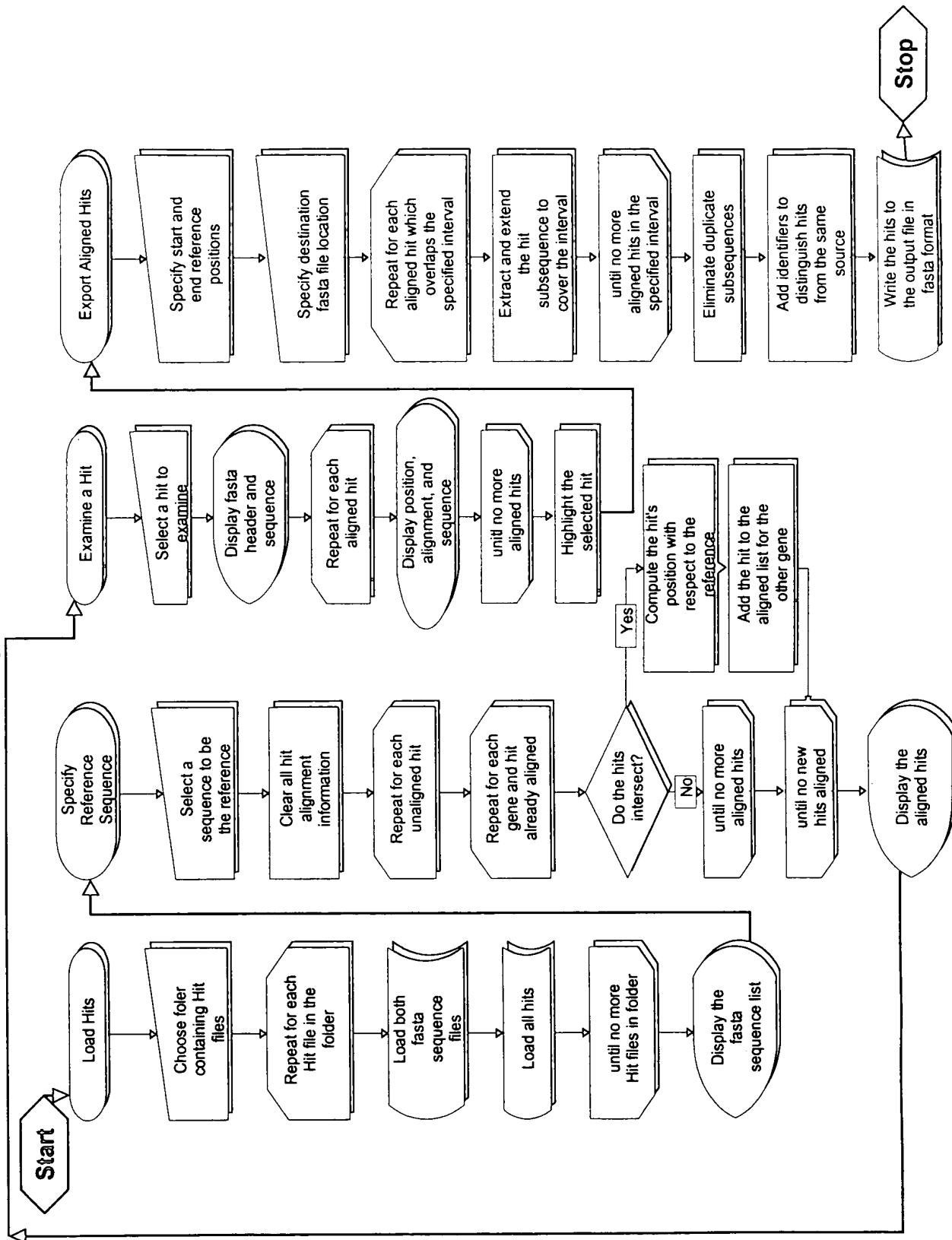
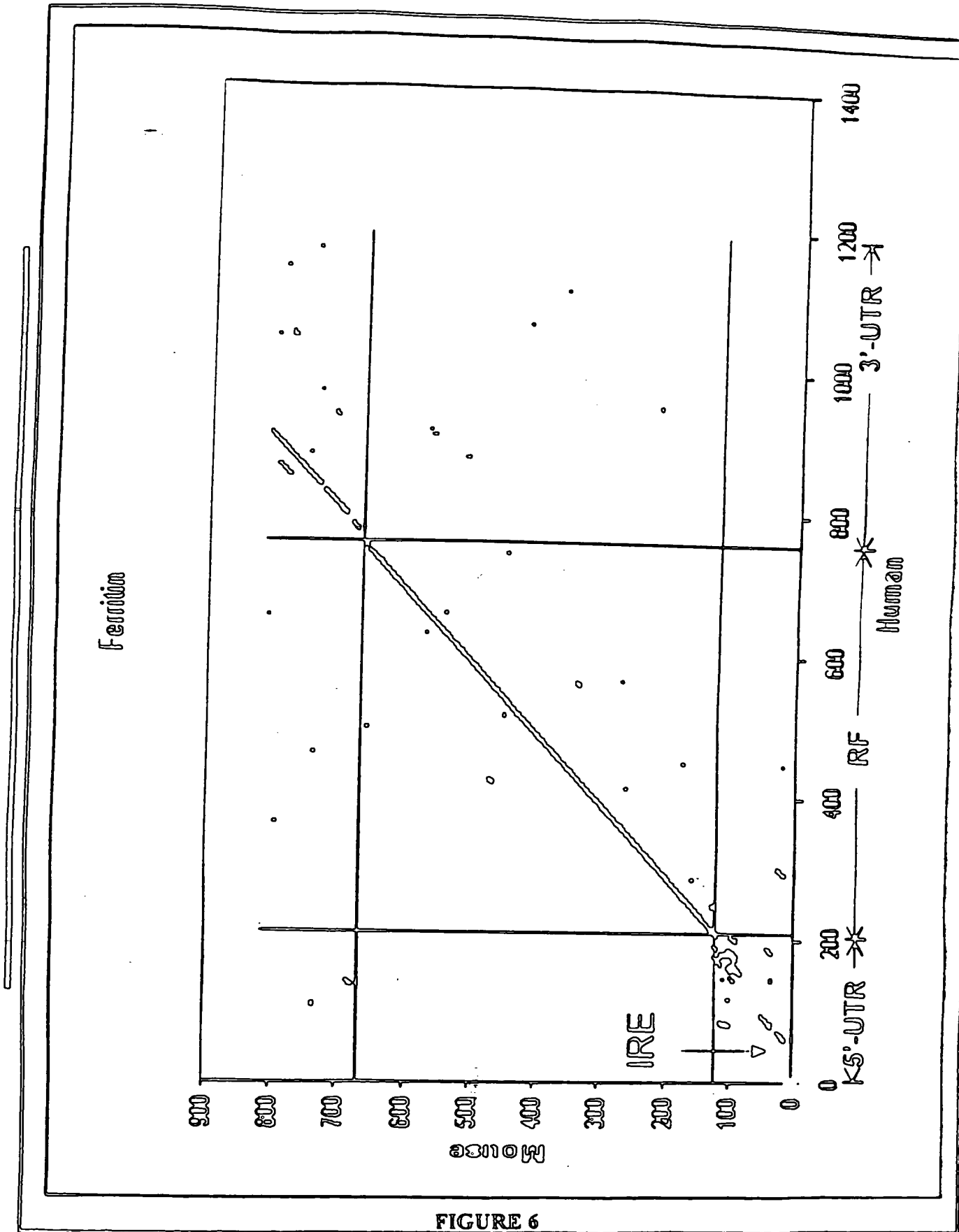


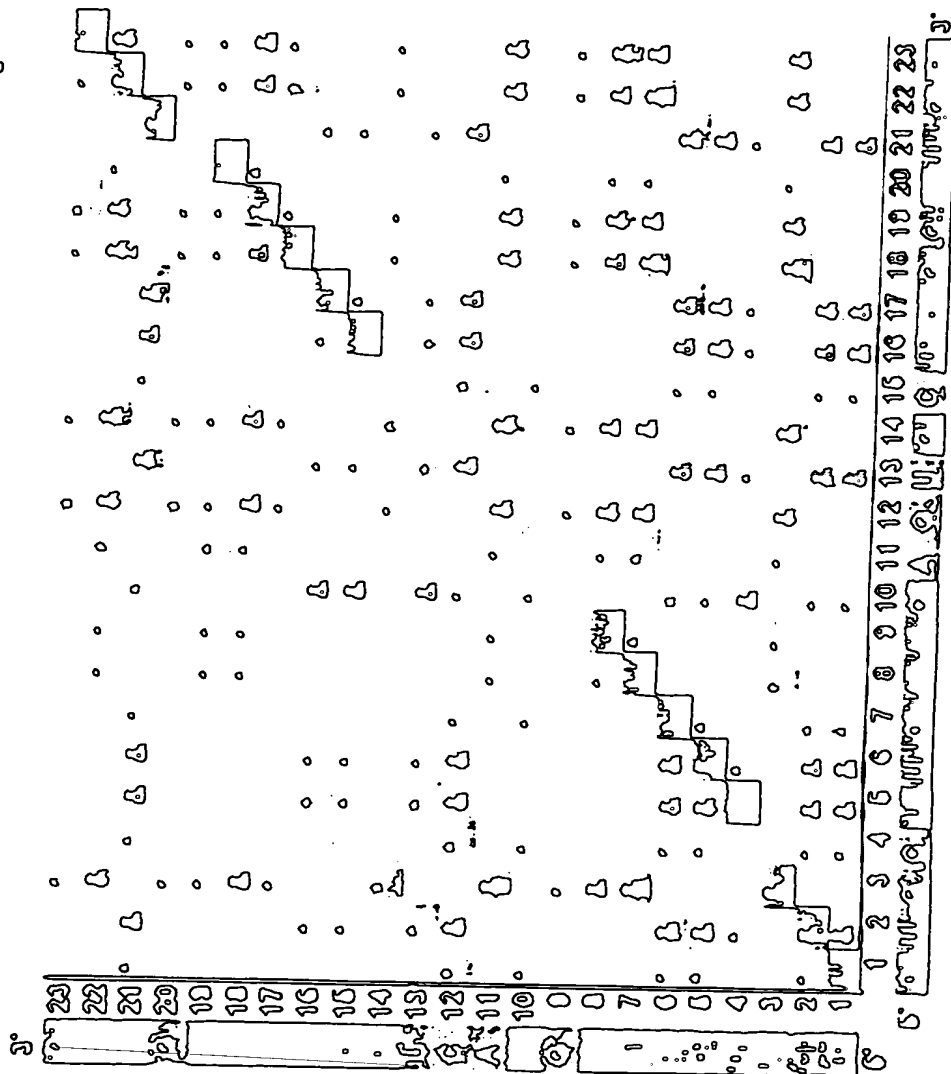
FIGURE 5C

Fig. 5D





Self Complementation Analysis - Single Sequence



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23

FIGURE 7

Self Complementarity Comparisons 13 ortholog overlay

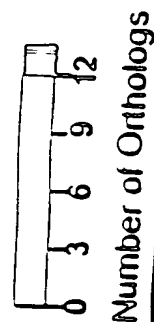
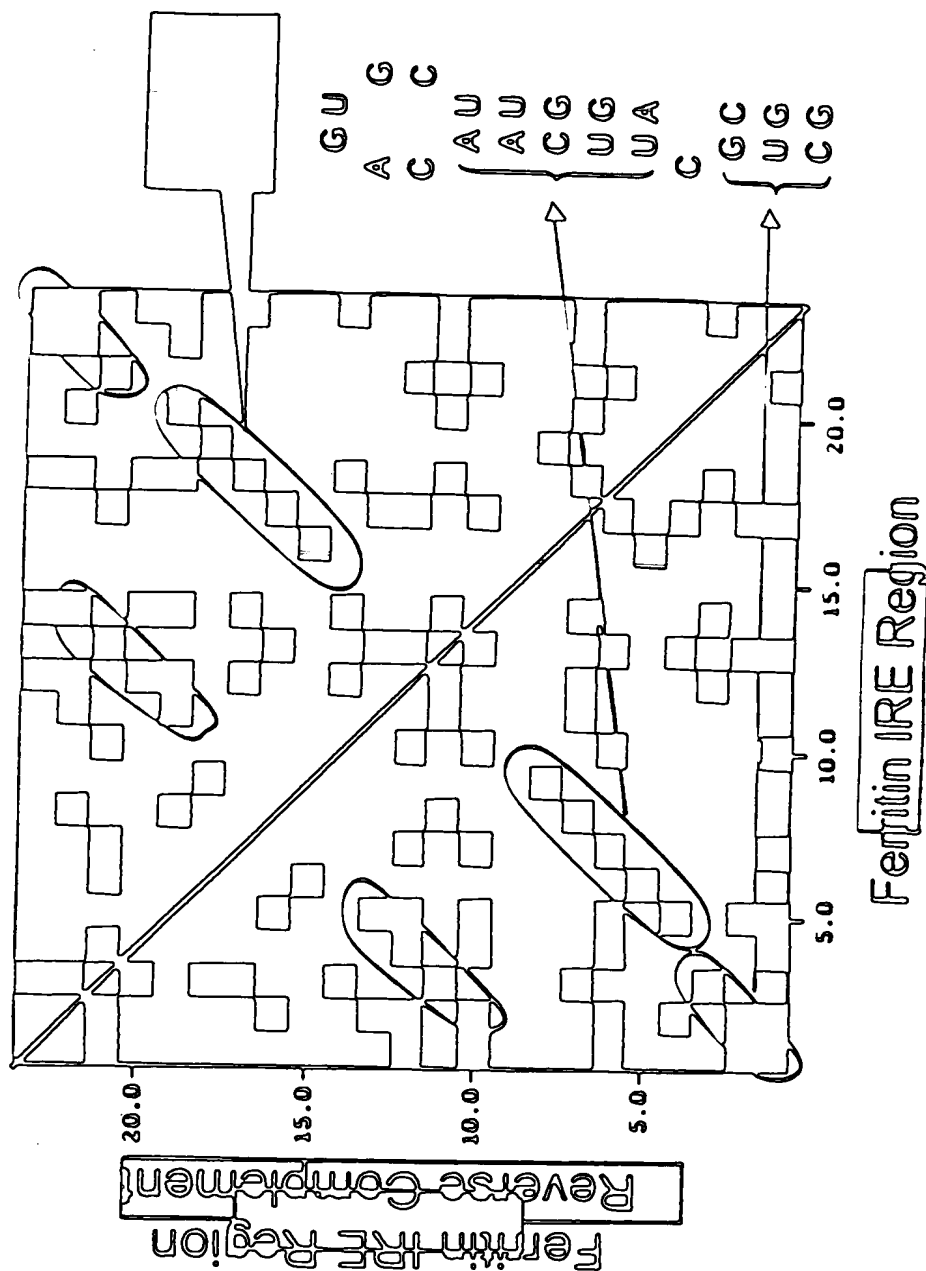
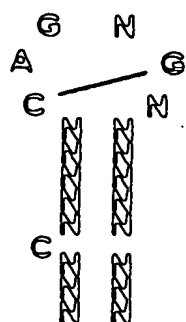


FIGURE 8

Typical Descriptor

This is an example of a descriptor used to identify iron response elements. To search the database using RNAMOT, the stem-loop model is converted to a text string as shown below:



IRE

Stem-loop
Model

H1 S1 H2 S2 H2 H1

H1 3:3 NNN:NNN

S1 1 C

H2 5:5 NNNNN:NNNNN

S2 6 CAGNGN

W2

M0

IRE String descriptor

This descriptor allows for a window (W) of 2 (allows G-U pairing) and no mismatch. N can be any nucleotide. H refers to the stem region while S refers to the single stranded region.

FIGURE 9

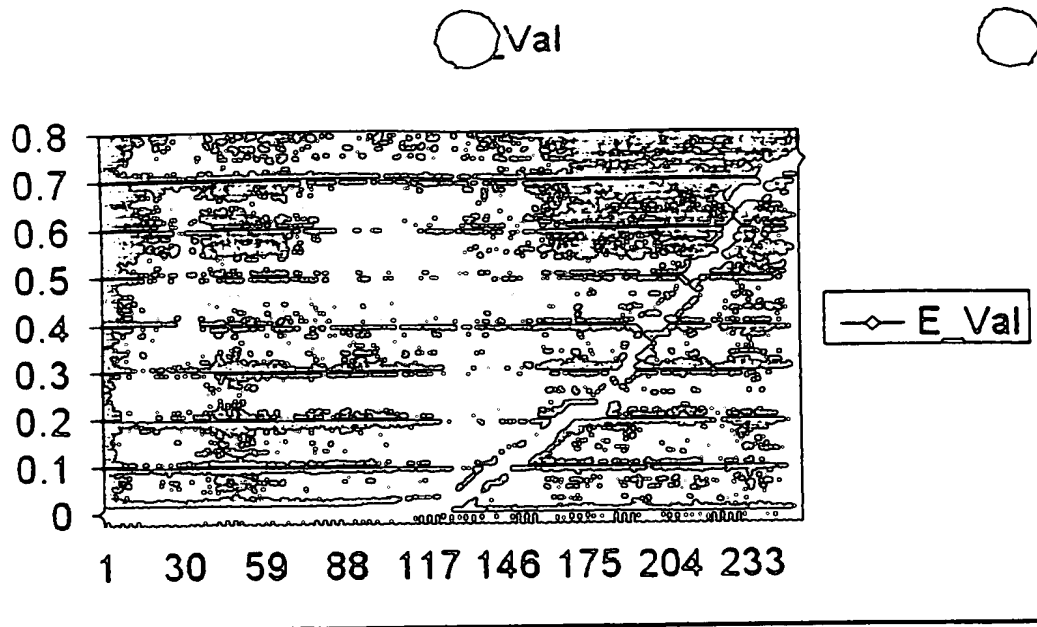


FIGURE 10

For the purpose of this study, the data was collected from the following sources:

Ferritin

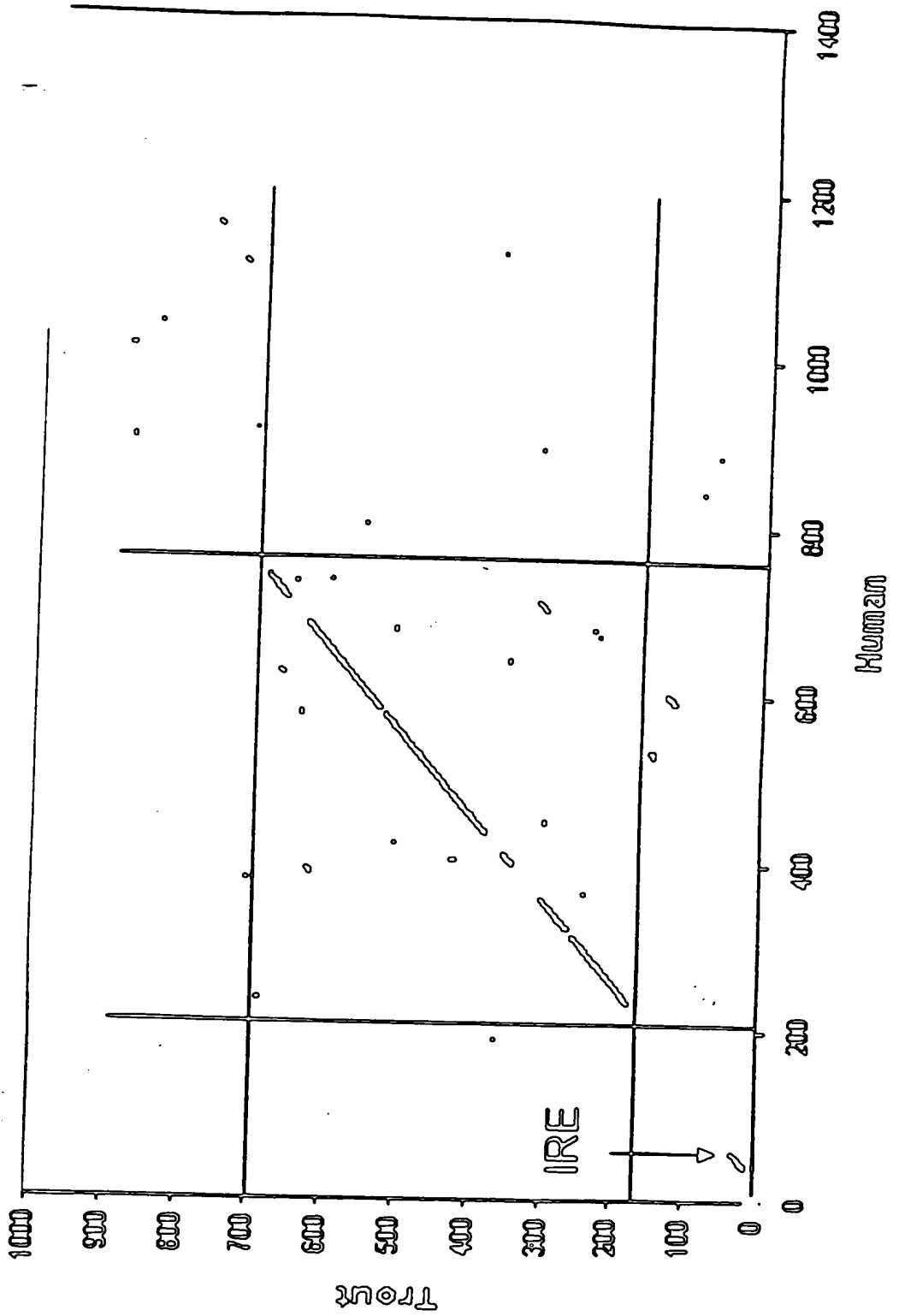


FIGURE 11

Ferris

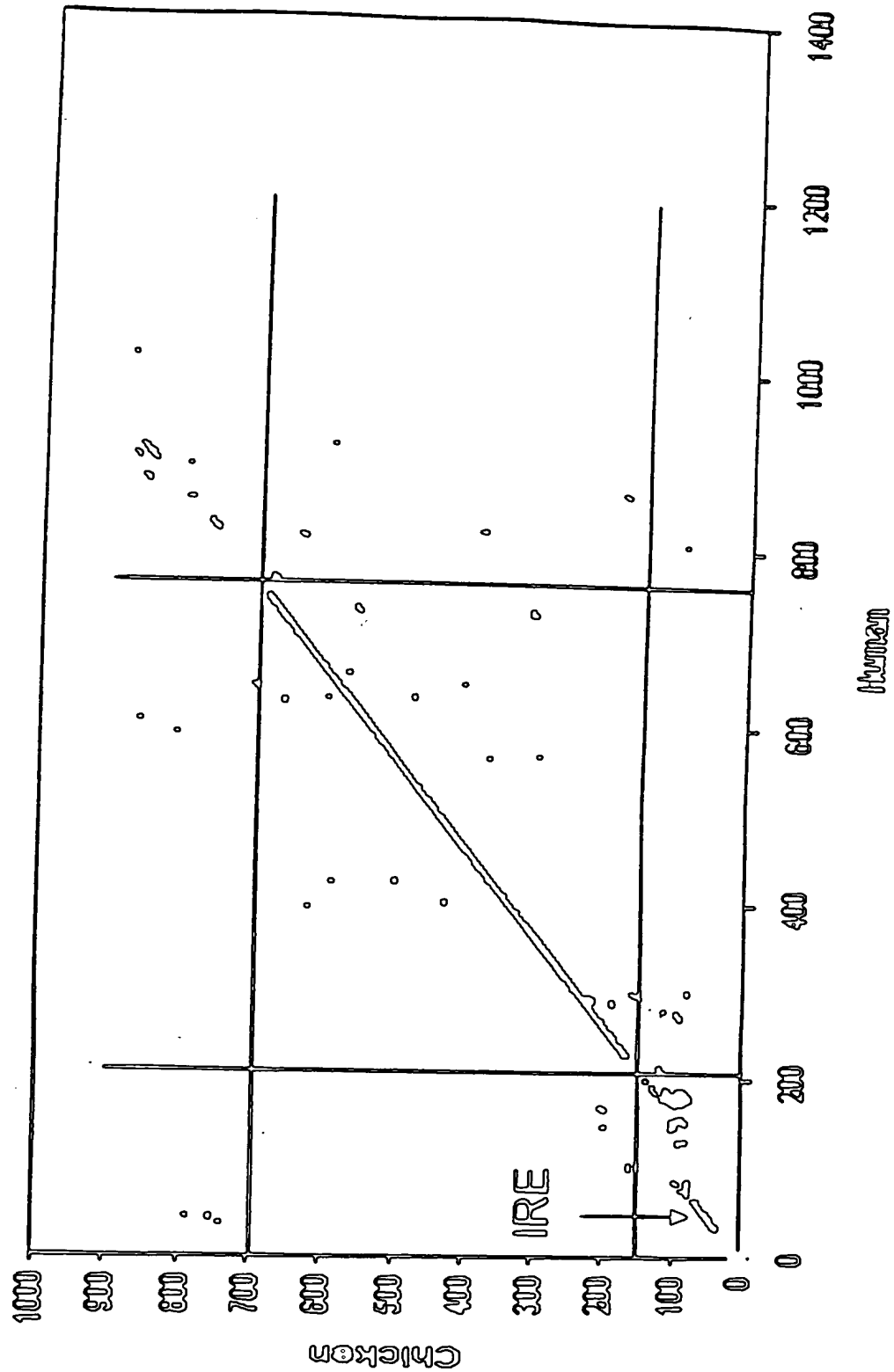
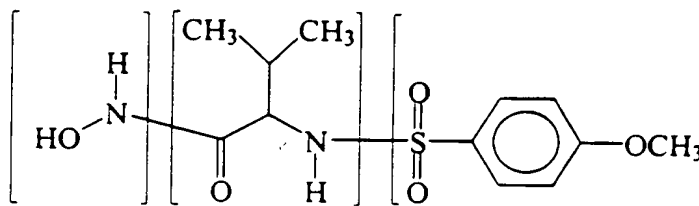
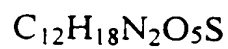
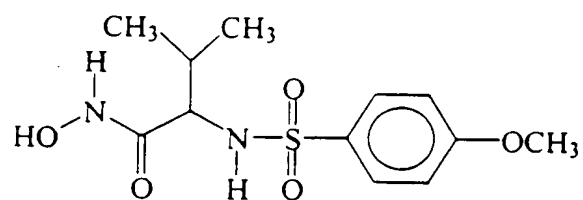


FIGURE 12

FIGURE 13

mosquit

Compound CI



	Fi	Fii	Fiii
Molecular formula	H ₂ NO	C ₅ H ₉ NO	C ₇ H ₇ O ₃ S

FIGURE 14

Addition of fragments to yield compounds

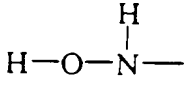
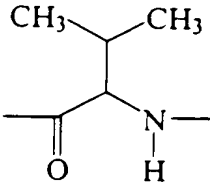
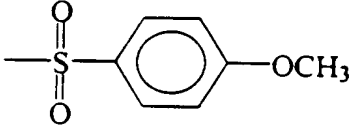
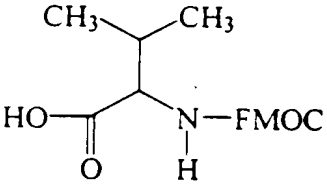
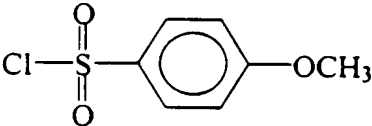
Fragment Identifier	Table			
	Structure	Name	Molecular formula	Other
F _i		Hydroxylamine	H ₂ NO	...
F _{ii}		Amino acid	C ₅ H ₉ NO	...
F _{iii}		Sulfonyl	C ₇ H ₇ O ₃ S	...

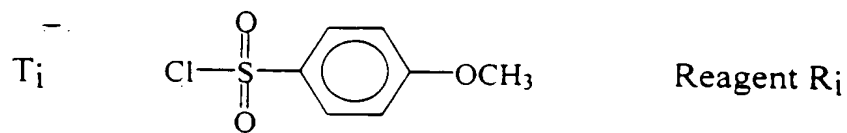
FIGURE 15

Reagents	Identifier	Name	Properties
$\text{H}-\text{O}-\text{NH}_2$ or $\textcircled{\text{P}}-\text{O}-\text{NH}_2$	R _i	Hydroxylamine	...
	R _{ii}	Fmoc blocked amino acid	...
	R _{iii}	Sulfonylchloride	...

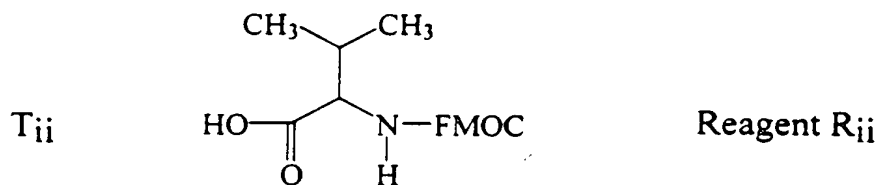
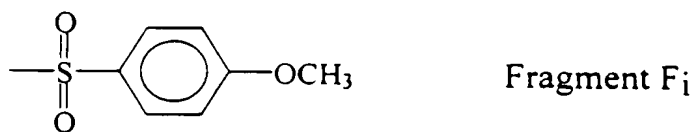
$\textcircled{\text{P}}$ = Solid support

FIGURE 16

Transformation



↓ reaction conditions alpha



↓ reaction conditions beta



↓ reaction conditions gamma



Ⓟ = Solid support

FIGURE 17

Common Fragment / Different Reagents and Transformations

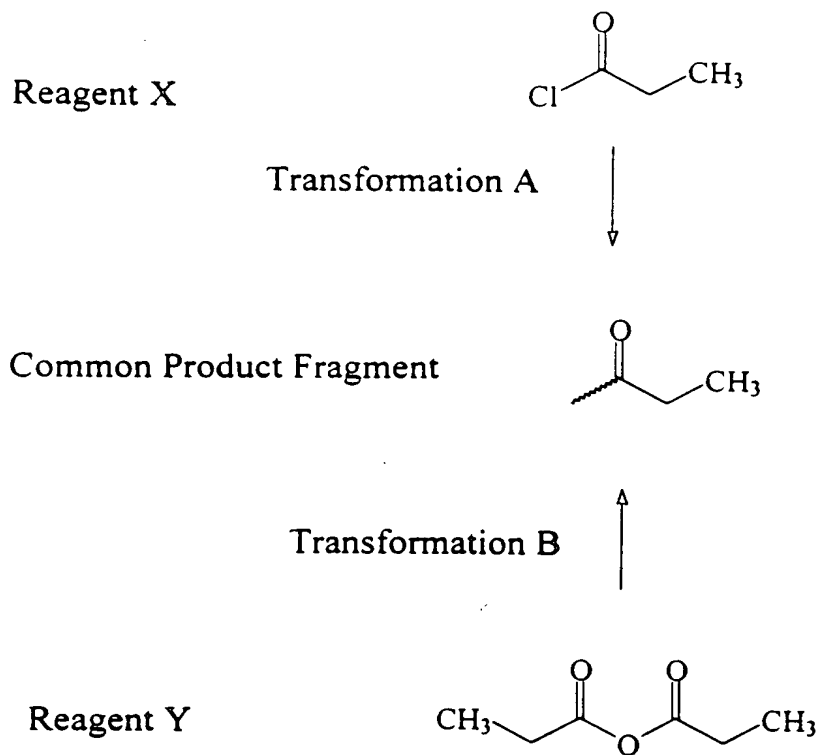


FIGURE 18

Common Fragment / Different Reagents and Transformations

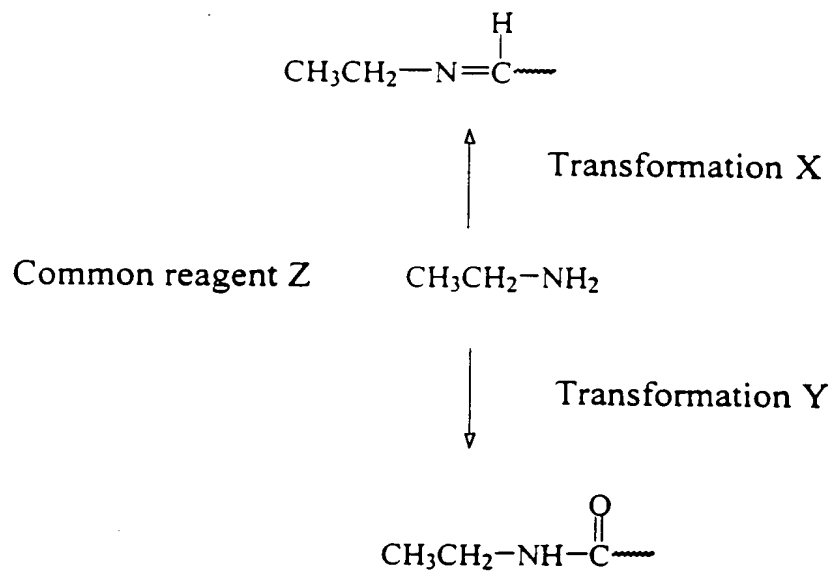


FIGURE 19A

Common Reagent

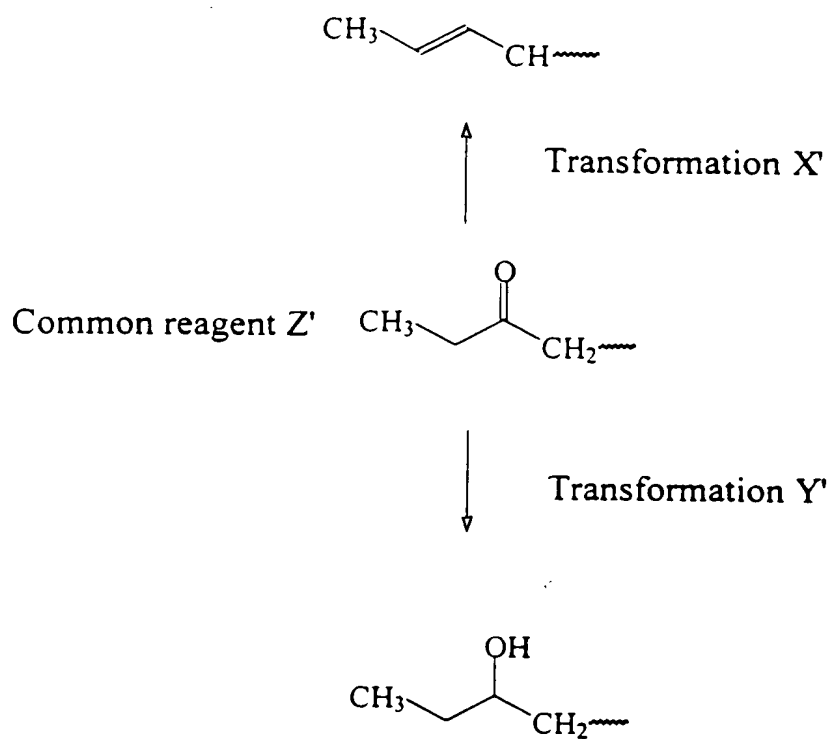
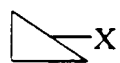


FIGURE 19B

Symbolic addition of fragments to yield compound

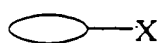
<u>Symbolic Structure</u>	<u>Symbolic Identifier</u>	<u>Molecular formula</u>
---------------------------	----------------------------	--------------------------

Fragment



F_i'

$C_uH_vN_w \dots$



F_{ii}'

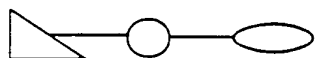
$C_uH_vN_w \dots$



F_{iii}'

$C_uH_vN_w \dots$

Compound



CI'

$C_uH_vN_w \dots$

Molecular formula F_i'

+

Molecular formula F_{ii}'

+

Molecular formula F_{iii}'

= Molecular formula CI'

FIGURE 20

Symbolic Reagent Table

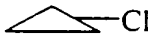
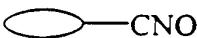
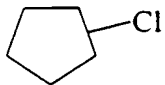
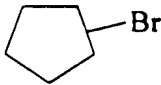
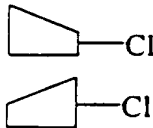
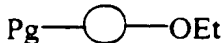

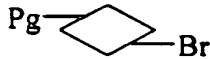
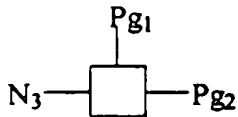
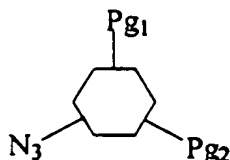
<u>Identifier</u>	<u>Name</u>	<u>Structure</u>	<u>Molecular formula</u>
R1	xxx		xxx
R2	...		...
R3	...		...
R4	...		...
R5	...		...
R6	...		...
R7	...		...
R8	...		...
R9	...		...
R10	...		...

FIGURE 21



Symbolic Fragment Table

<u>Identifier</u>	<u>Symbolic Structure</u>	<u>Molecular formula</u>	<u>Molecular Weight</u>
F1		xxx	xxx
F2	
F3	
F4	
F5	
F6	
F7	
F8	

FIGURE 22

Symbolic Transformation Table

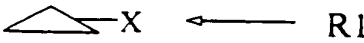
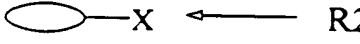
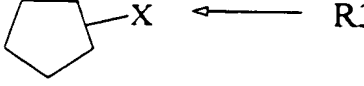
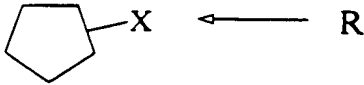
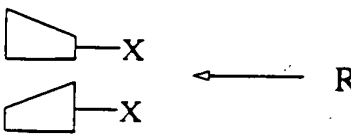



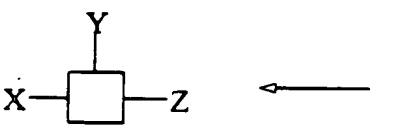
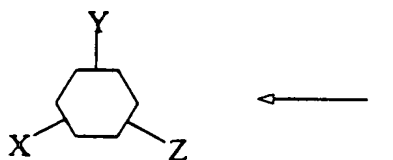
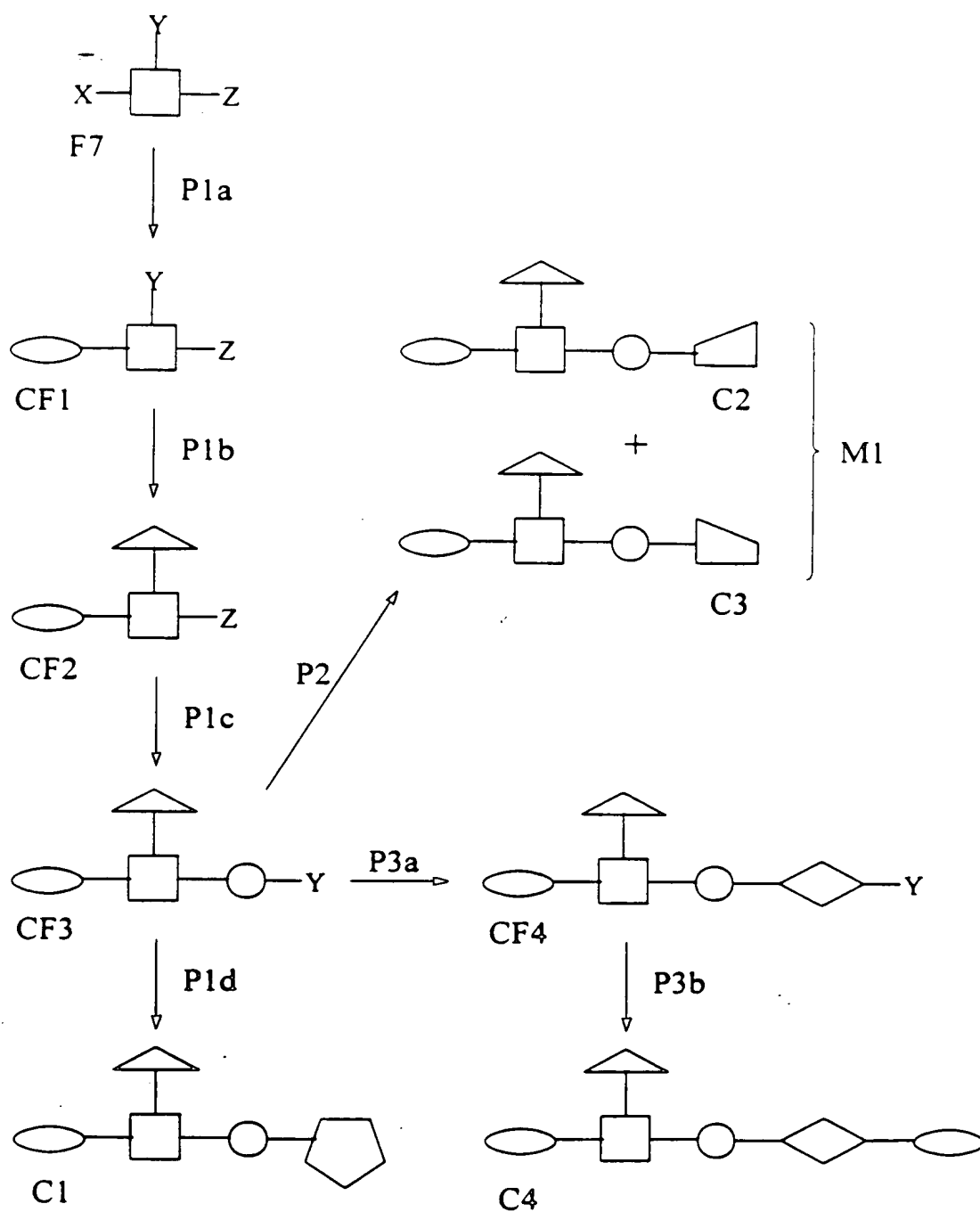
<u>Identifier</u>		<u>Symbolic Reactions</u>	<u>Reagent</u>
T1	F1	 $\triangle - X \leftarrow R1$	conditions α
T2	F2	 $\text{Oval} - X \leftarrow R2$	conditions β
T3	F3	 $\text{Pentagon} - X \leftarrow R3$	conditions α
T4	F3	 $\text{Pentagon} - X \leftarrow R4$	conditions α
T5	F4	 $\begin{matrix} \text{Trapezoid} - X \\ \text{Trapezoid} - X \end{matrix} \leftarrow R5$	conditions α
T6	F5	 $X - \text{Circle} - Y \leftarrow R6$	conditions ϵ
T7	F5	 $X - \text{Circle} - Y \leftarrow R7$	conditions α
T8	F6	 $X - \text{Diamond} - Y \leftarrow R8$	conditions α
T9	F7	 $X - \text{Square} - Z \text{ with } Y \text{ on top} \leftarrow R9$	conditions γ
T10	F8	 $X - \text{Hexagon} - Z \text{ with } Y \text{ on top} \leftarrow R10$	conditions γ

FIGURE 23

Single Compounds and Mixtures



P = synthetic path **CF** = complex fragment
F = fragment **M** = mixture
C = compound

FIGURE 24



Mixture 2

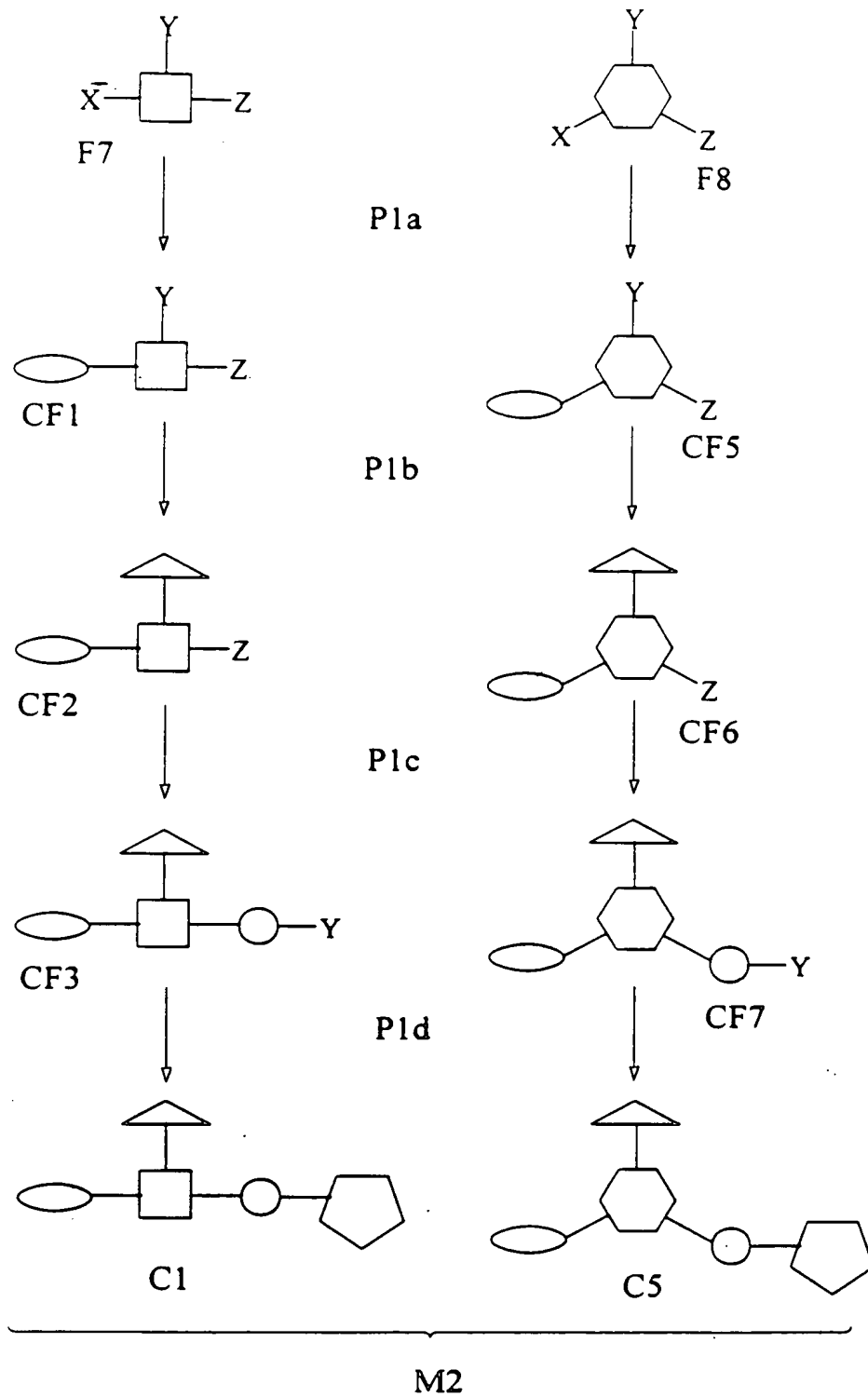


FIGURE 25

Mixture 3

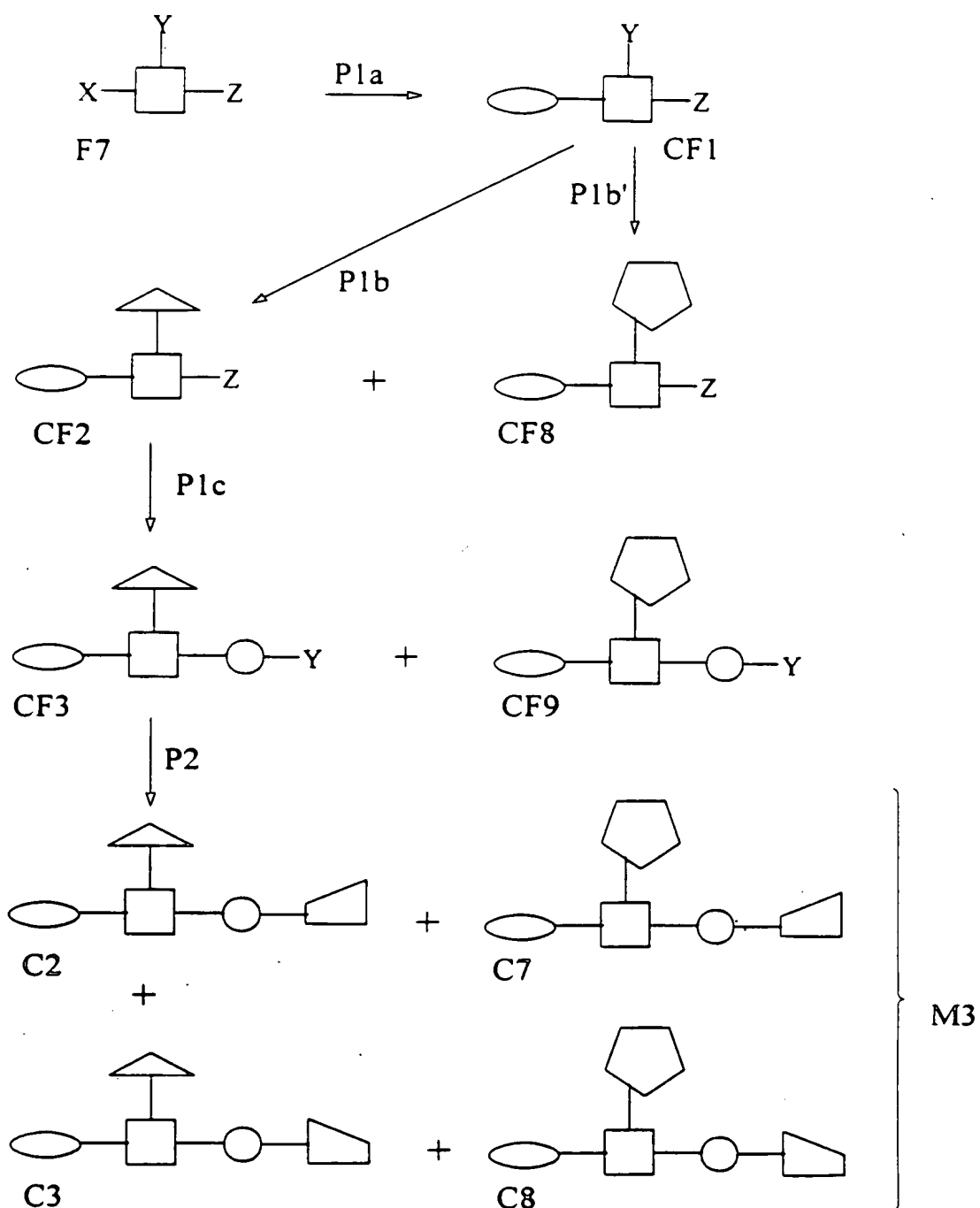
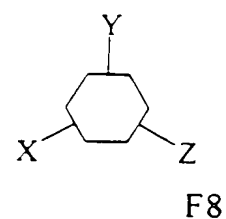
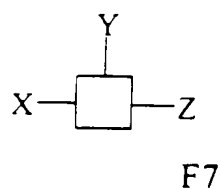
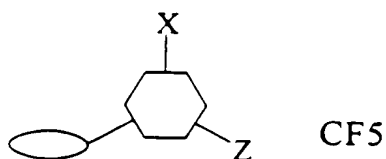
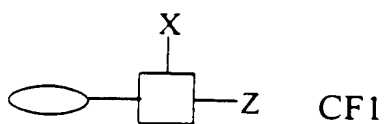


FIGURE 26

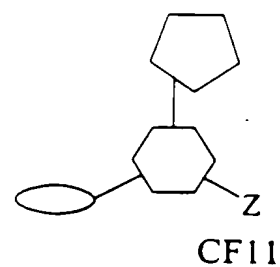
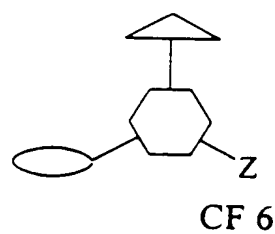
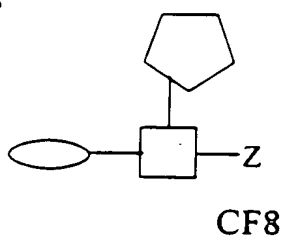
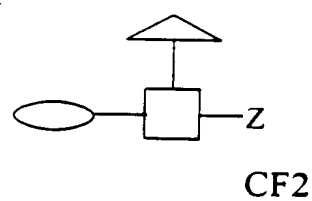
Mixture 4
2 Starting Fragments



2 Complex Fragments



4 Complex Fragments



8 Complex Fragments

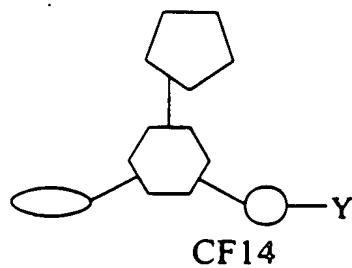
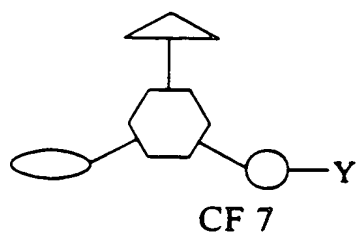
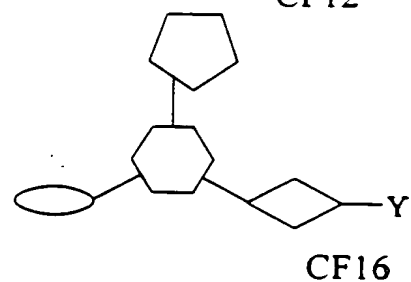
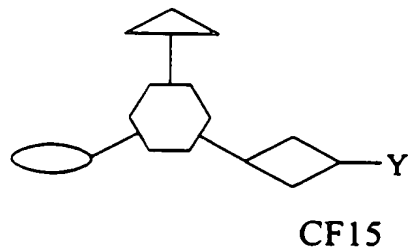
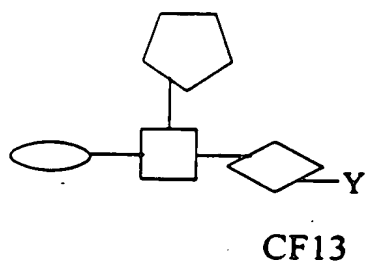
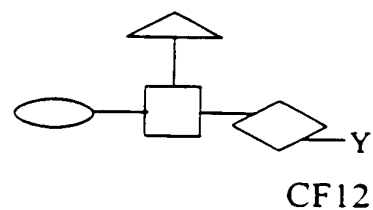
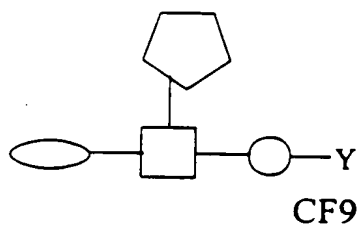
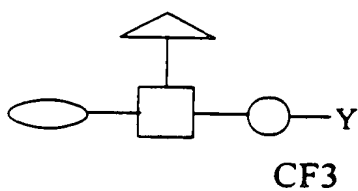


FIGURE 27A

Mixture 4 (continued)

16 compounds

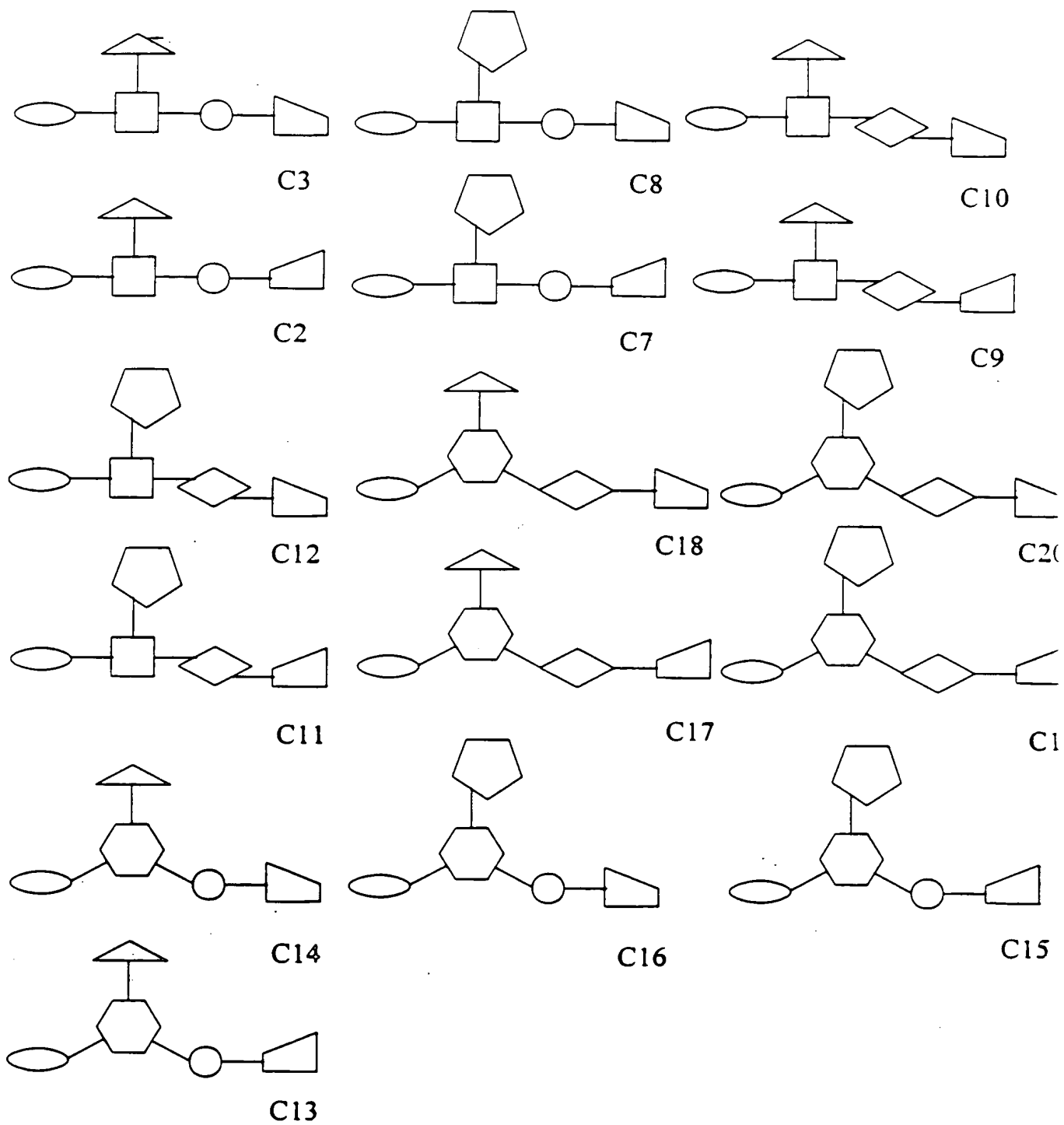


FIGURE 27B

Tracking Table for Compound C1

(a) By Fragments:

n	n+1	n+2
F7	F2 F1 F5	F3

(b) By Transformations:

Synthesis Path 1

n	n+1	n+2
T9	T2 T1 T6	T3

Synthesis Path 2

n	n+1	n+2
T9	T2 T1 T7	T3

Synthesis Path 3

n	n+1	n+2
T9	T2 T1 T6	T4

Synthesis Path 4

n	n+1	n+2
T9	T2 T1 T7	T4

FIGURE 28

Tracking Table

Tracking M1

Step 1

T9		
----	--	--

Step 2

T9	T2	
----	----	--

Step 3

T9	T2 T1	
----	----------	--

Step 4

T9	T2 T1 T7	
----	----------------	--

Step 5

T9	T2 T1 T7	T5 ¹
----	----------------	-----------------

C2

Step 5

T9	T2 T1 T7	T5 ²
----	----------------	-----------------

C3

FIGURE 29



Tracking M2

Step 1

n	n+1	n+2
T9		

Step 1

n	n+1	n+2
T10		

Step 2

n	n+1	n+2
T9	T2	

Step 2

n	n+1	n+2
T10	T2	

Step 3

n	n+1	n+2
T9	T2 T1	

Step 3

n	n+1	n+2
T10	T2 T1	

Step 4

n	n+1	n+2
T9	T2 T1 T7	

Step 4

n	n+1	n+2
T10	T2 T1 T7	

Step 5

n	n+1	n+2
T9	T2 T1 T7	T4

Step 5

n	n+1	n+2
T10	T2 T1 T7	T4

C1

C5

FIGURE 30

Tracking Table

Tracking M3

Step 1

T9		

Step 2

T9		
	T2	

Step 3

T9		
	T2	
	T1	

Step 3

T9		
	T2	
	T3	

Step 4

T9		
	T2	
	T1	
	T7	

Step 4

T9		
	T2	
	T3	
	T7	

Step 5

T9		
	T2	
	T1	
	T7	
		T5 ¹
		C2

Step 5

T9		
	T2	
	T1	
	T7	
		T5 ²
		C3

Step 5

T9		
	T2	
	T3	
	T7	
		T5 ¹
		C7

Step 5

T9		
	T2	
	T3	
	T7	
		T5 ²
		C8

FIGURE 31

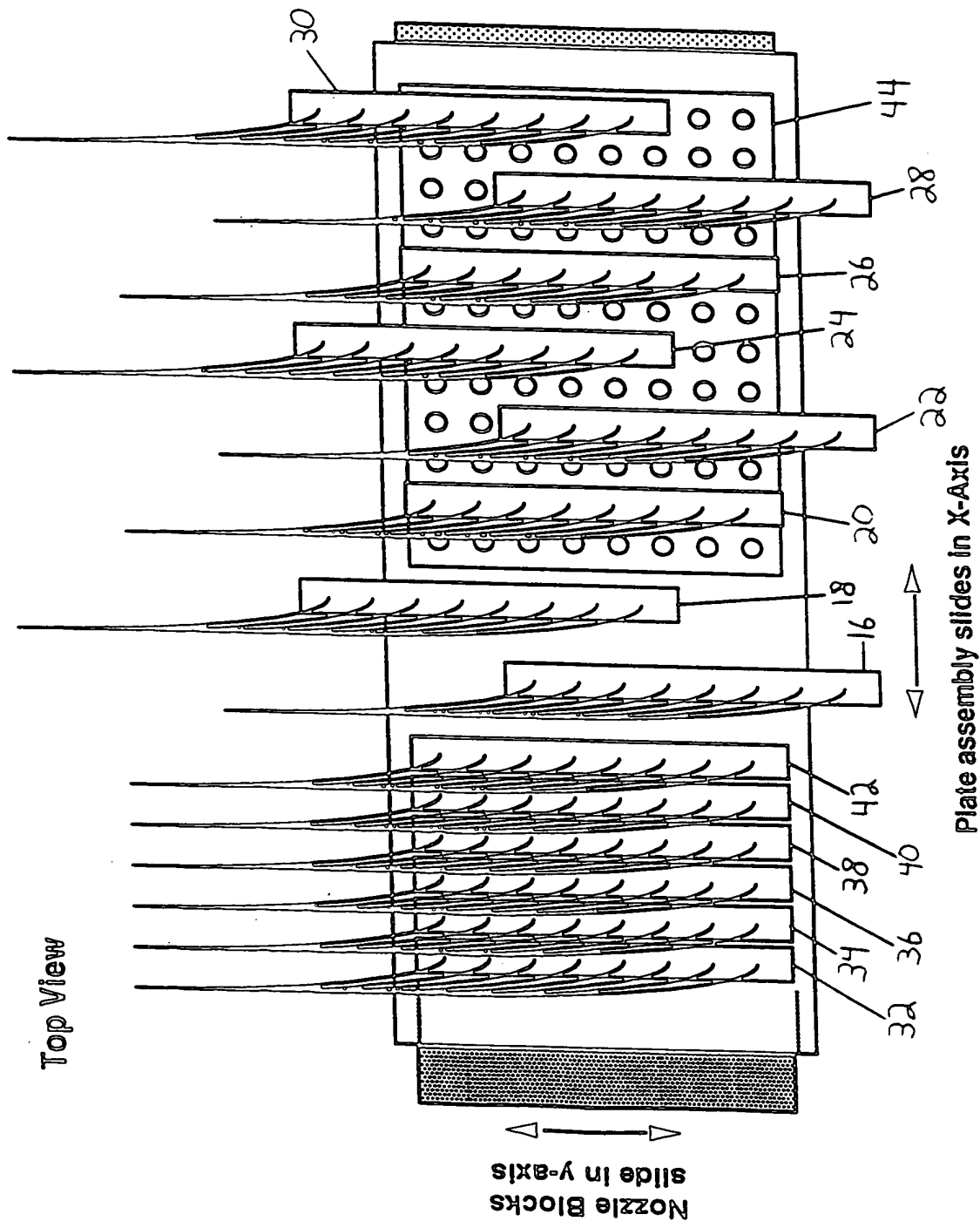


FIGURE 33

Synthesis of hydroxamic acids from alcohol resin

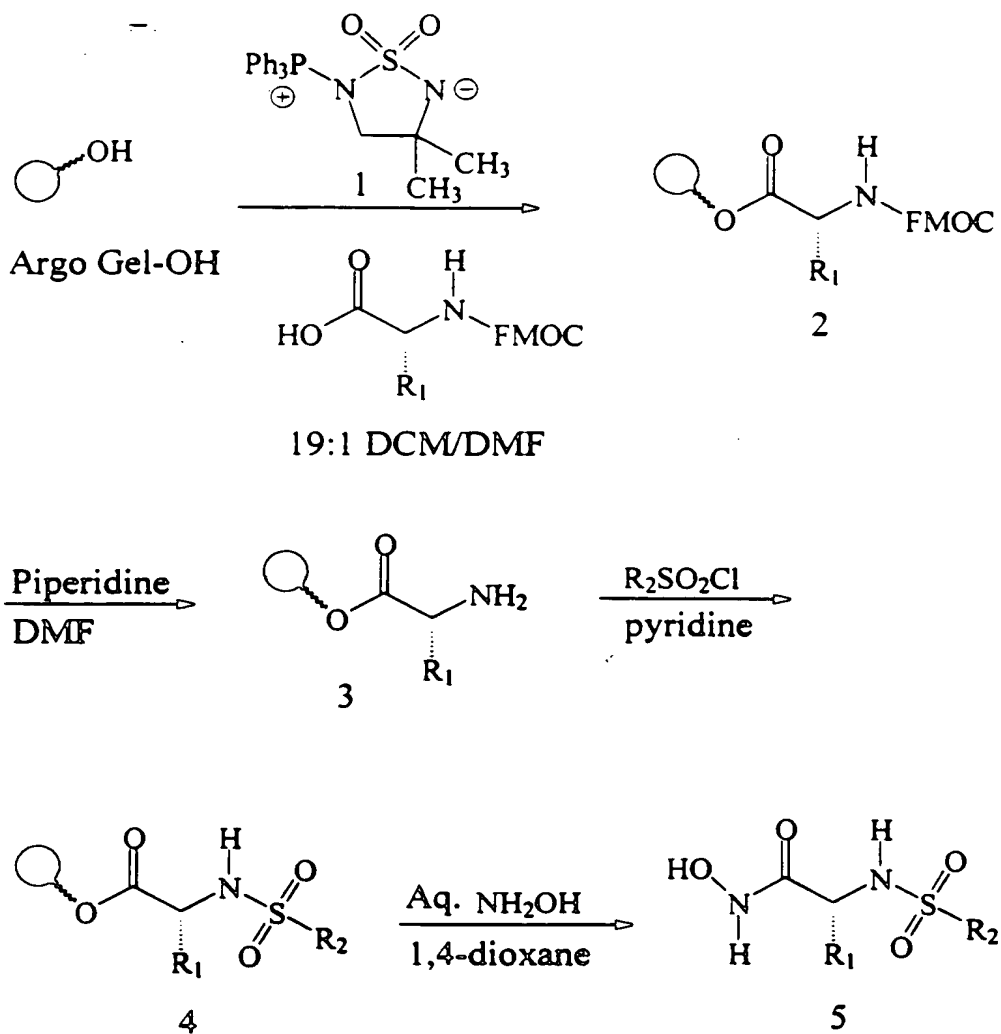


FIGURE 34

Synthesis of hydroxamic acids from hydroxylamine resin

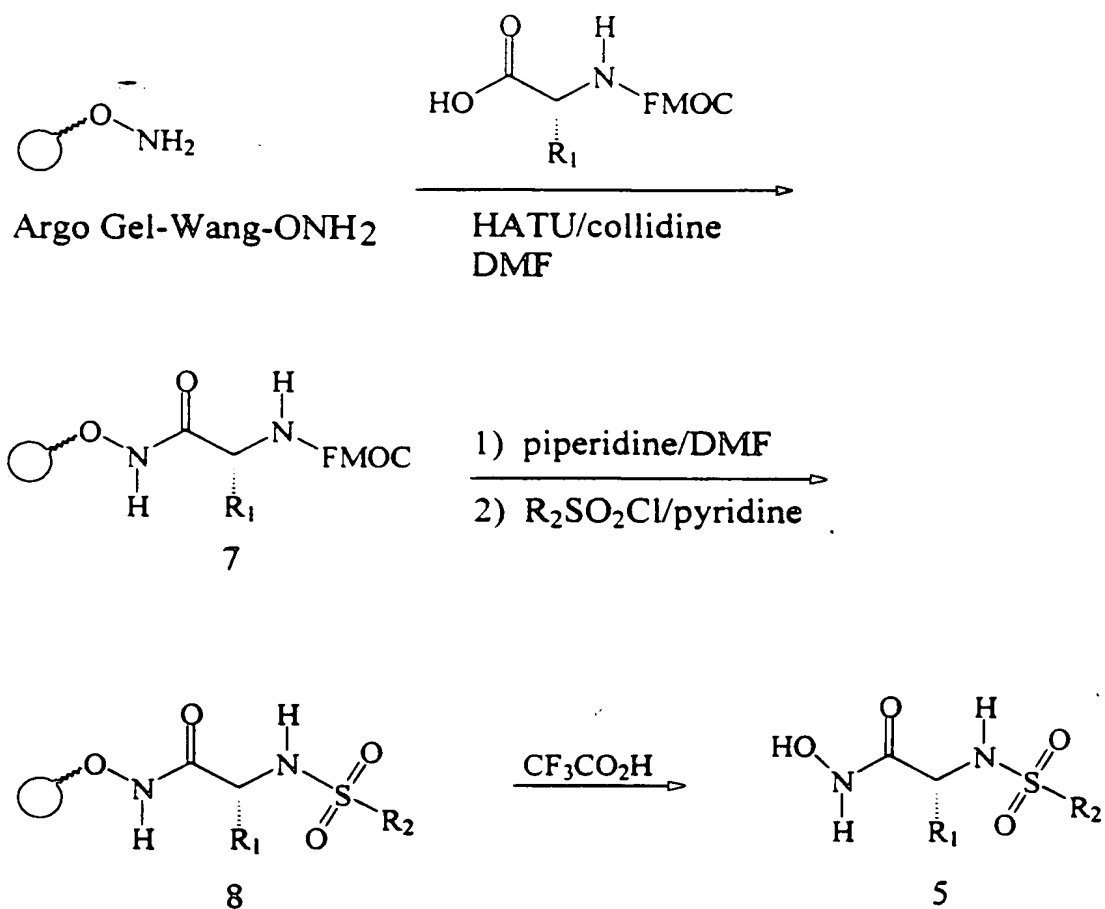


FIGURE 35

Biological Activity and Binding Energy for Structures Docked to TAR with Solvation/Desolvation Energy

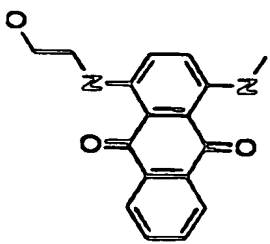
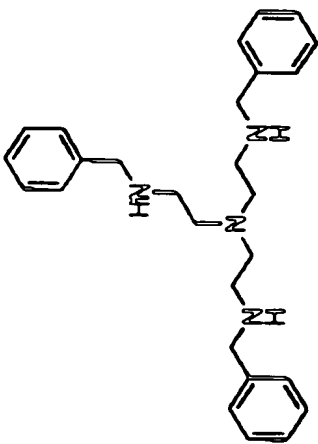
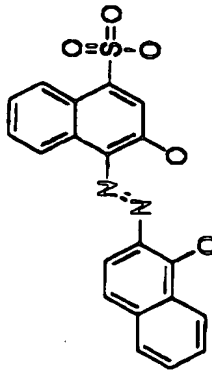
ACD Code	Structure	Calc. ΔG of binding (kcal/mole)	IC ₅₀ (μ M)
00001199		-5.1	<2
00192509		-8.5	<2
00003934		-5.1	<50

FIGURE 37

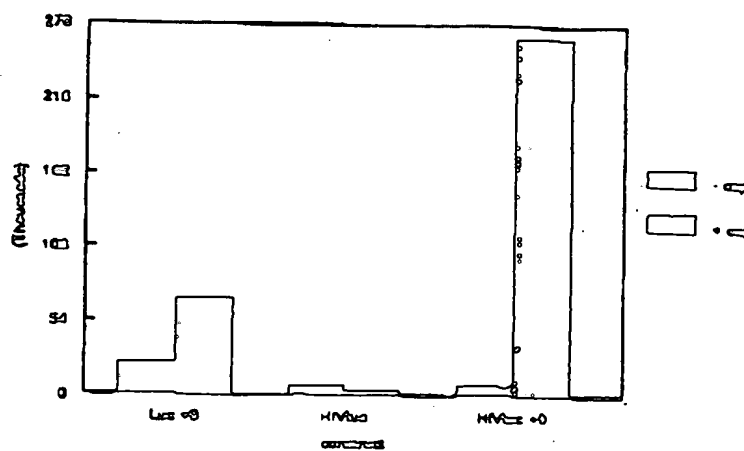


FIGURE 38A

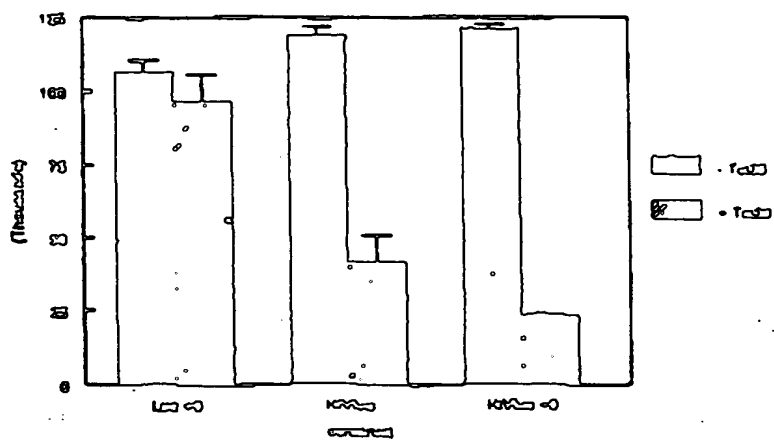


FIGURE 38B

Variable	Mean	Standard deviation	Minimum	Maximum	Skewness	Kurtosis	Normality test
Age	35.2	12.5	20	65	0.15	3.2	0.98
Gender	0.5	0.5	0	1	-0.05	3.0	0.99
Marital status	0.7	0.5	0	1	-0.1	3.1	0.99
Education	12.5	2.5	9	16	0.2	3.3	0.97
Income	1500	500	500	3000	0.3	3.4	0.96
Health	0.8	0.4	0	1	-0.2	3.2	0.98
Stress	4.5	1.5	1	7	0.4	3.5	0.95
Depression	3.2	1.2	1	5	0.3	3.4	0.96
Life satisfaction	5.8	1.0	4	7	-0.1	3.1	0.99
Resilience	6.5	1.5	4	8	-0.2	3.2	0.98
Optimism	6.2	1.2	4	8	-0.1	3.1	0.99
Self-efficacy	6.8	1.0	5	8	-0.1	3.1	0.99
Emotional stability	6.0	1.2	4	8	-0.2	3.2	0.98
Life satisfaction	5.8	1.0	4	7	-0.1	3.1	0.99
Resilience	6.5	1.5	4	8	-0.2	3.2	0.98
Optimism	6.2	1.2	4	8	-0.1	3.1	0.99
Self-efficacy	6.8	1.0	5	8	-0.1	3.1	0.99
Emotional stability	6.0	1.2	4	8	-0.2	3.2	0.98

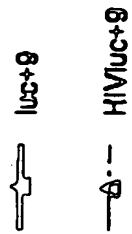


FIGURE 39

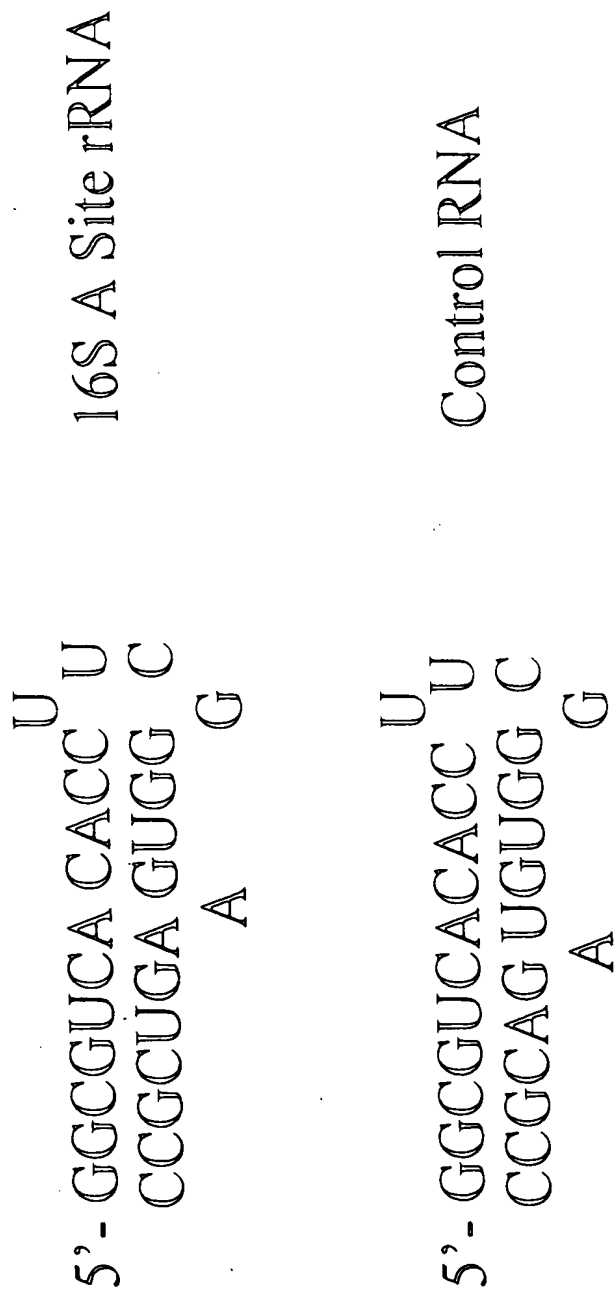


FIGURE 40 Sequence and structure of 27mer RNA target

MS/MS spectra of control RNA/DNA (upper) and control + paromomycin (lower) samples. The x-axis represents the mass-to-charge ratio (m/z) from 800 to 1900, and the y-axis represents relative abundance from 0 to 100. The upper spectrum shows a base peak at m/z 1005.9. The lower spectrum shows a base peak at m/z 1900.0.

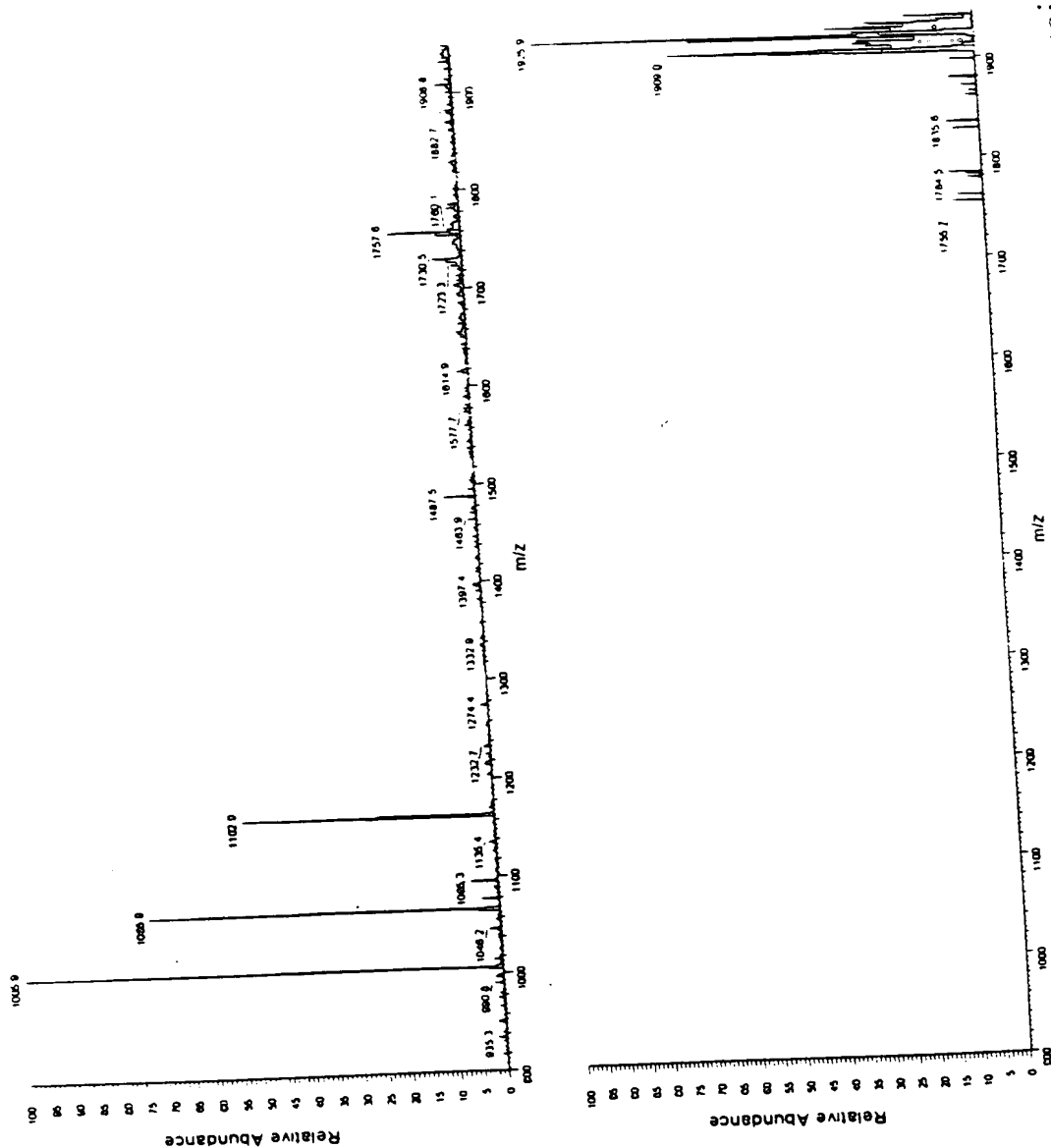


FIGURE 41 MS/MS of control RNA/DNA (upper); control+paromomycin (lower)

100% relative abundance from 1100 to 1120 m/z. The x-axis is labeled m/z and the y-axis is labeled Relative Abundance.

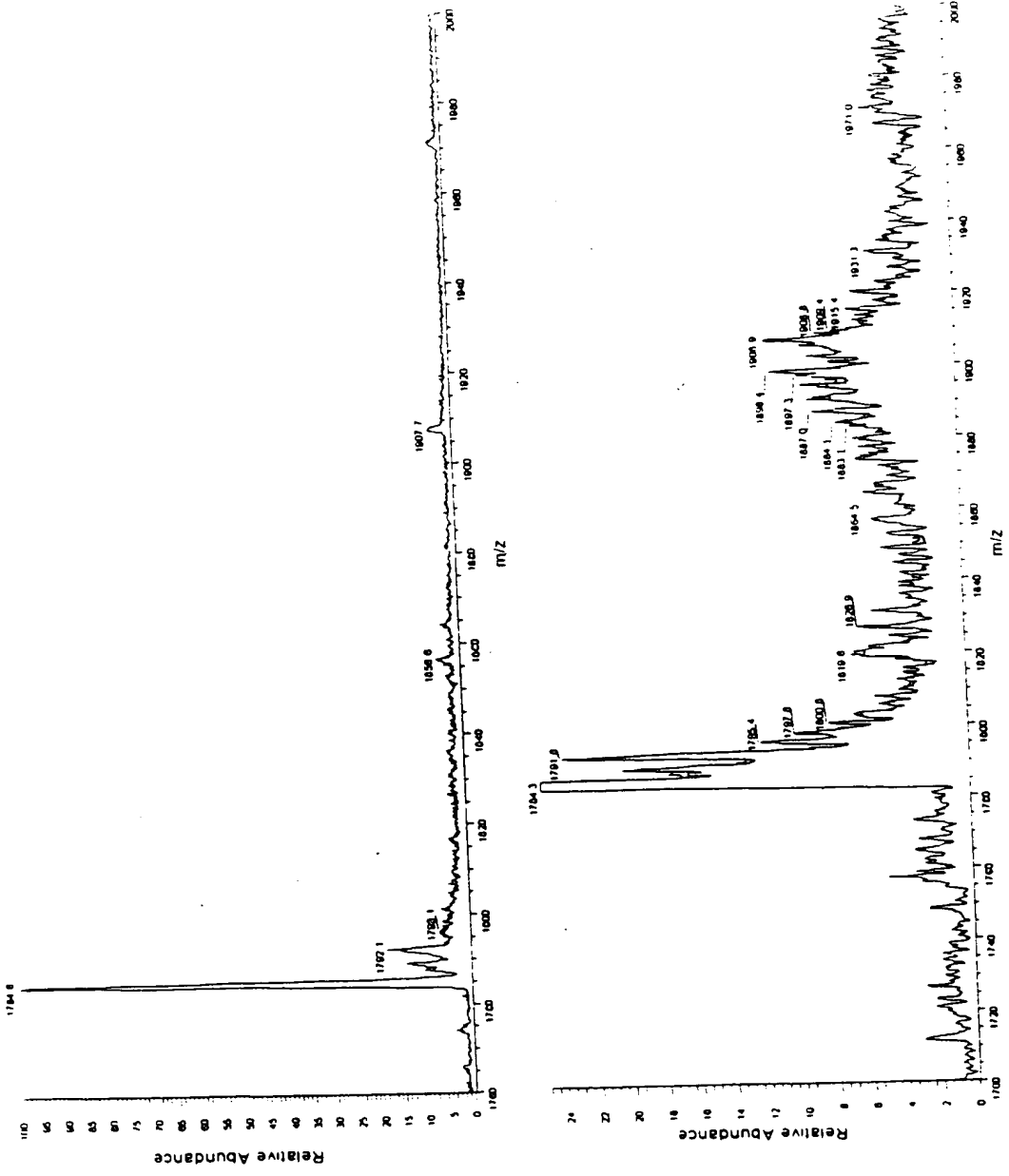


FIGURE 42 RNA/DNA chimera+paramomycin (upper); chimera+library (lower)

FIGURE 43
MS-MS analysis of member bound to RNA/DNA chimera

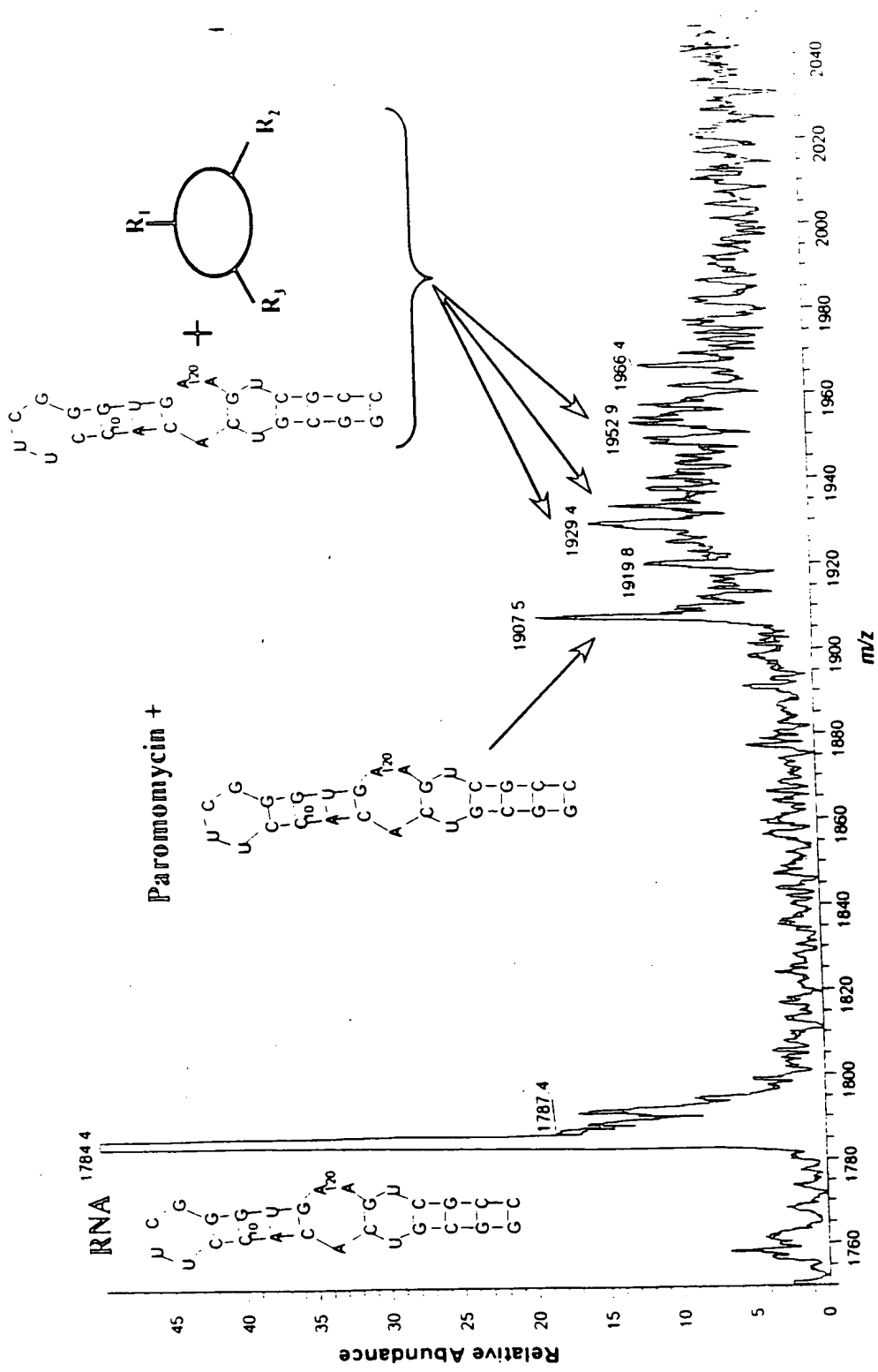


FIGURE 44 ESI-MS of RNA/DNA chimera bound to paromomycin and library

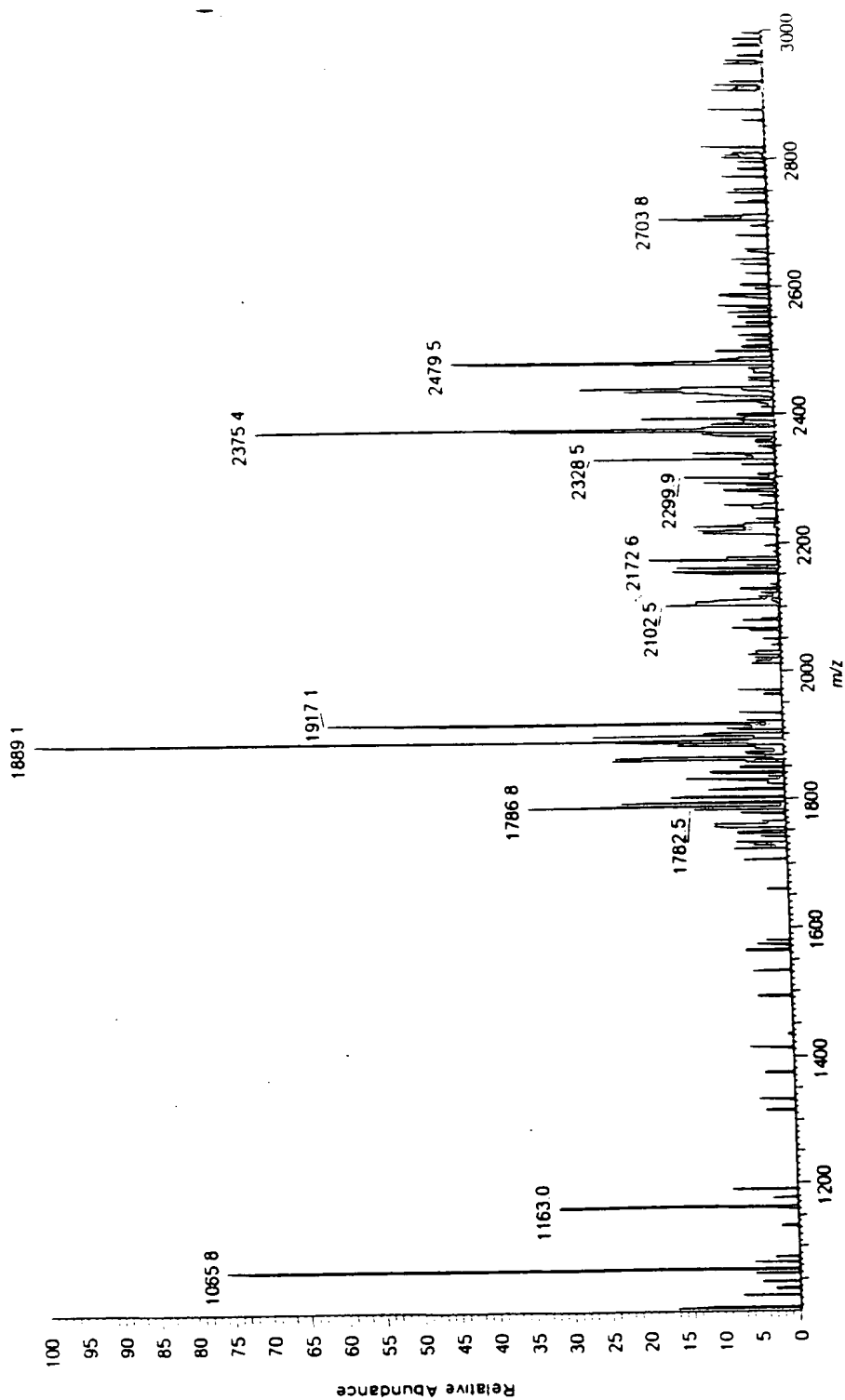


FIGURE 45 MS/MS of RNA/DNA chimera + compound with mass 665.1 not bound at the A-site

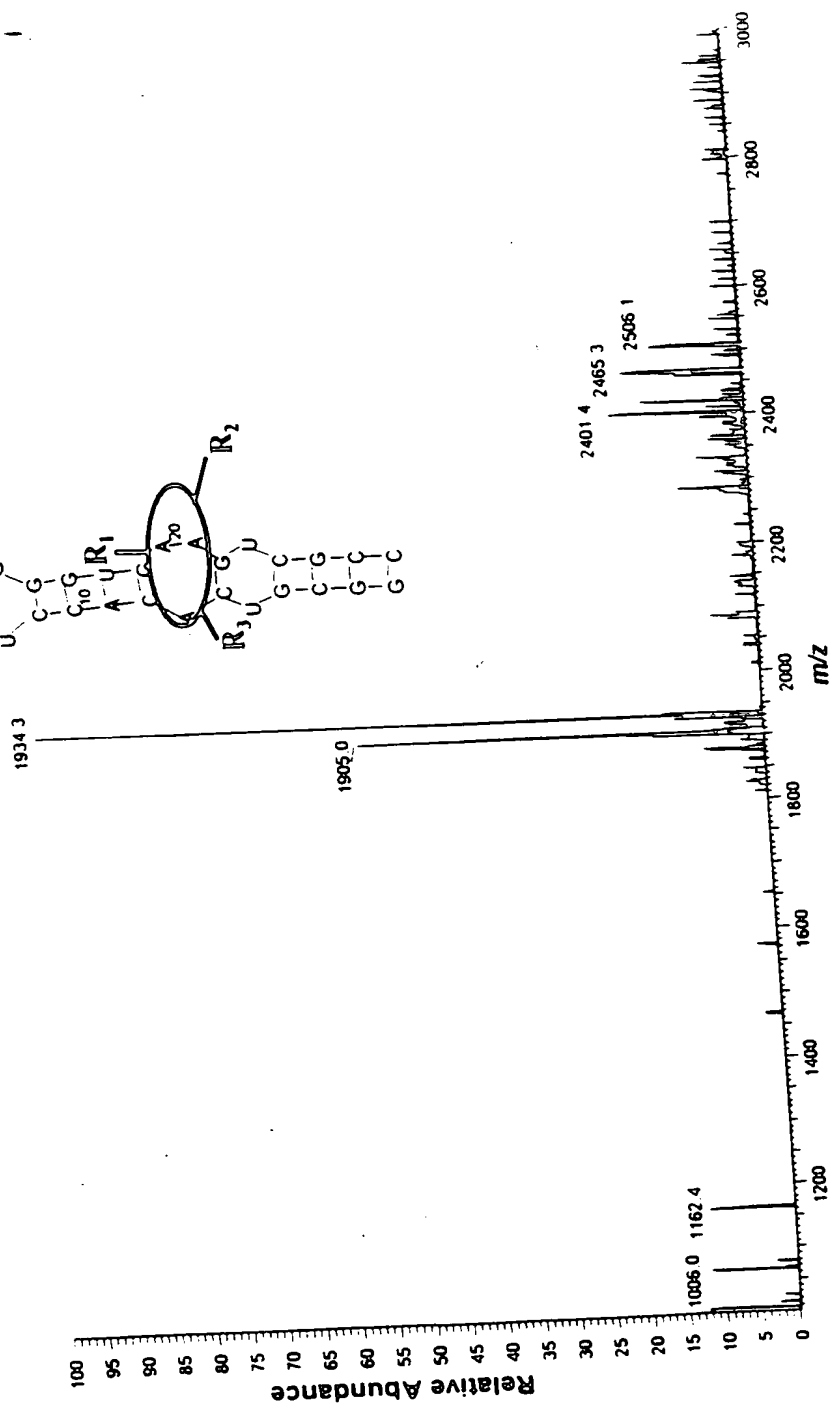


FIGURE 46
MS-MS analysis of member bound to RNA/DNA chimera at the A-Site



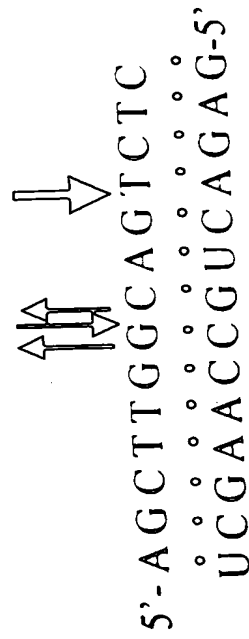
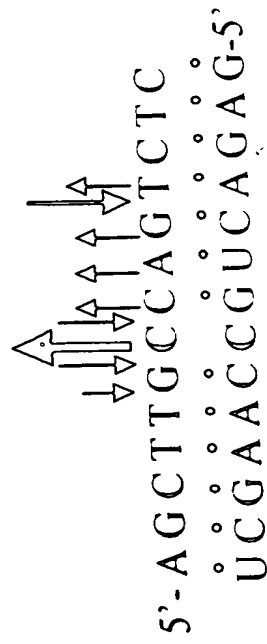
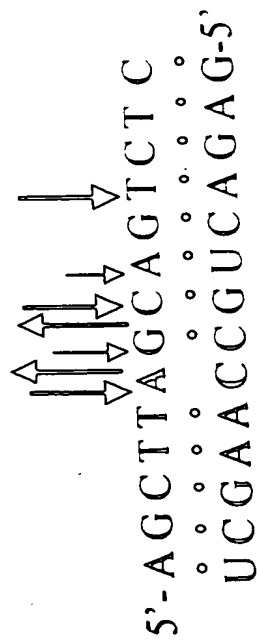
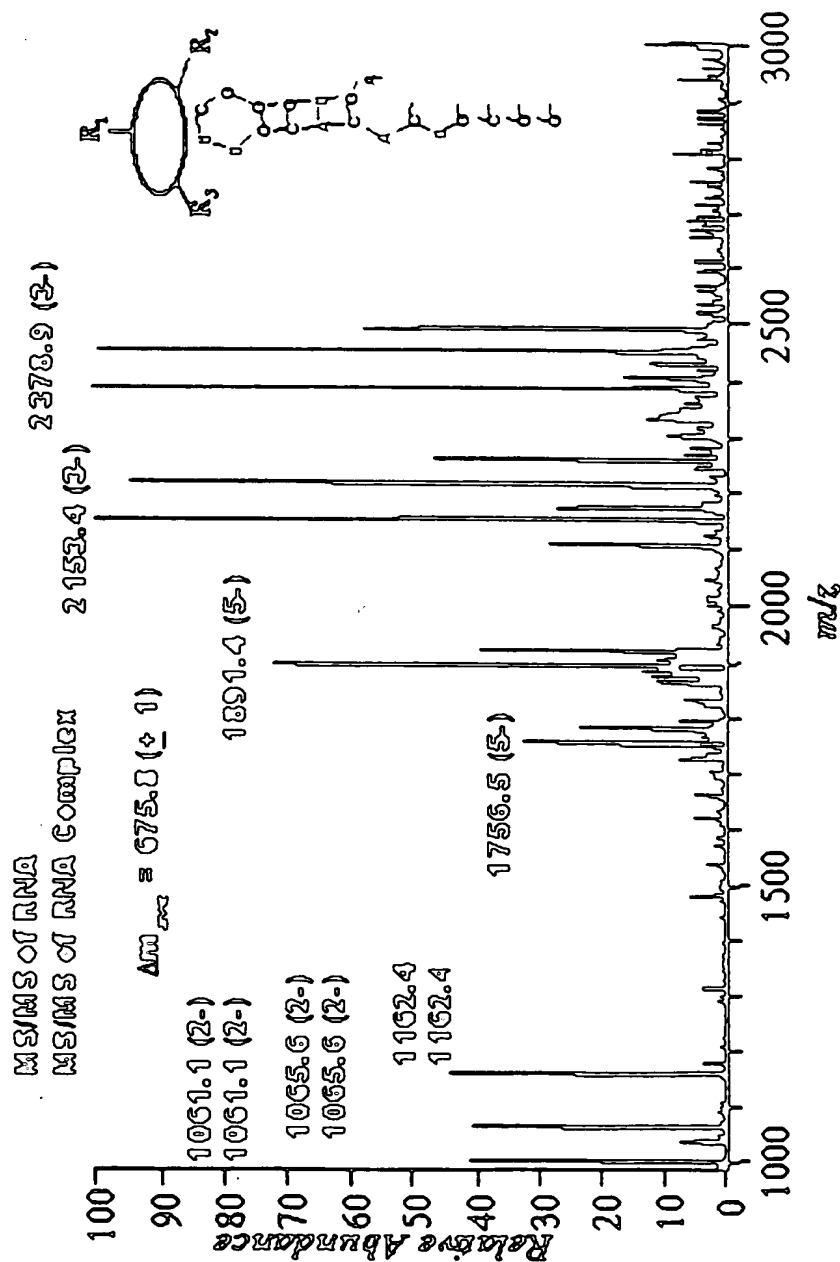
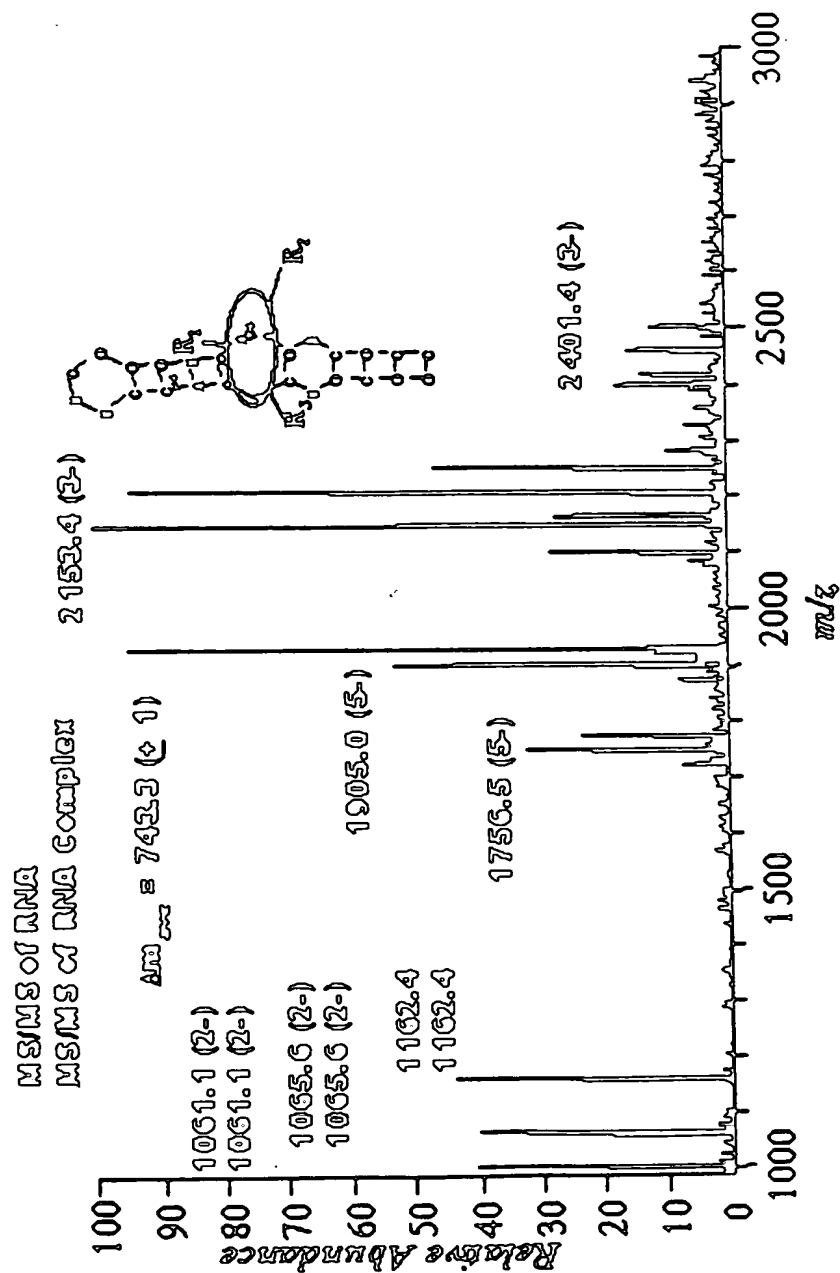


FIGURE 48
MS Fragmentation of DNA:RNA duplexes



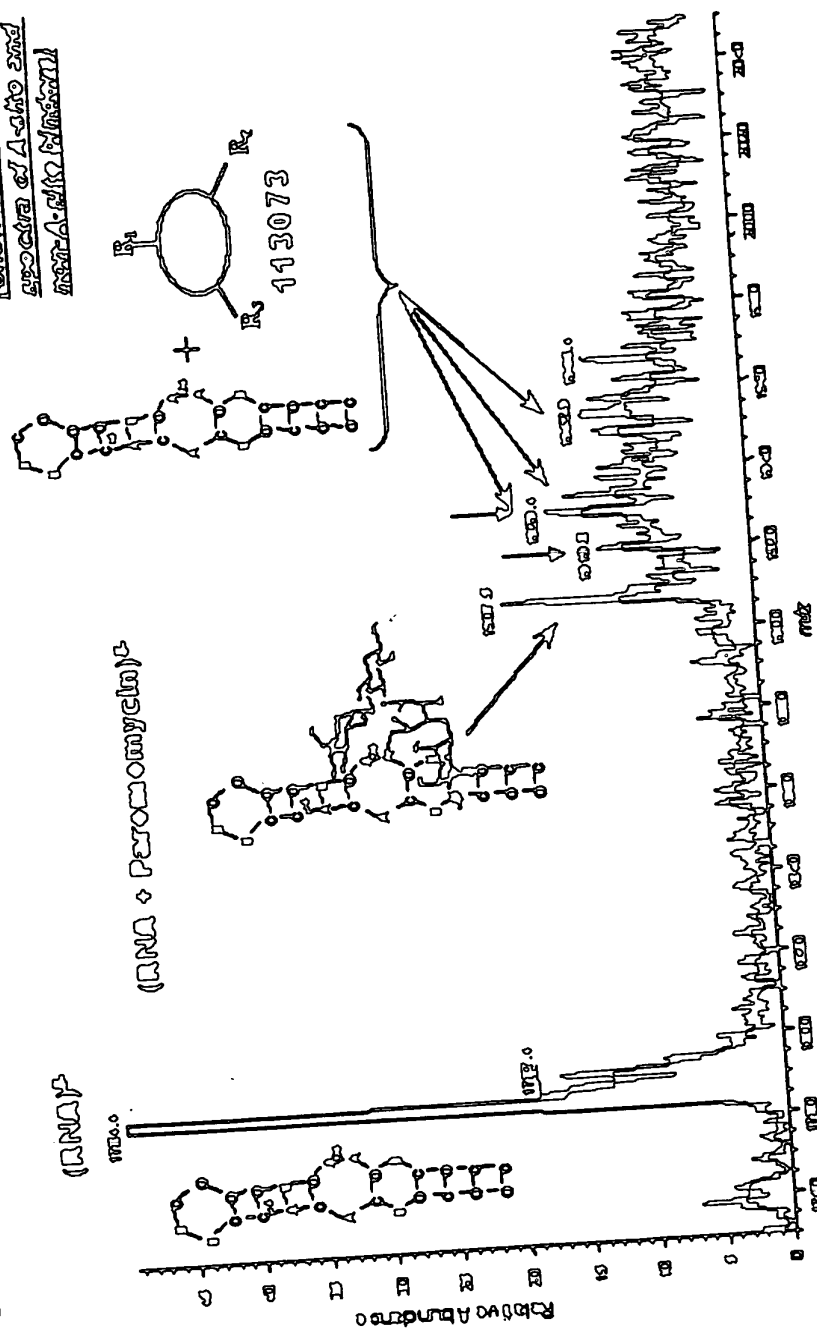
non-A site binder



MASS analysis of 16S A site RNA plus 216 member library

FIGURE 51

WAGNER, JAMES V.
BORN OCT 7 1908
SMITHSONIAN MUSEUM



Use of unbound RNA as internal mass standard provides low ppm mass measurement errors

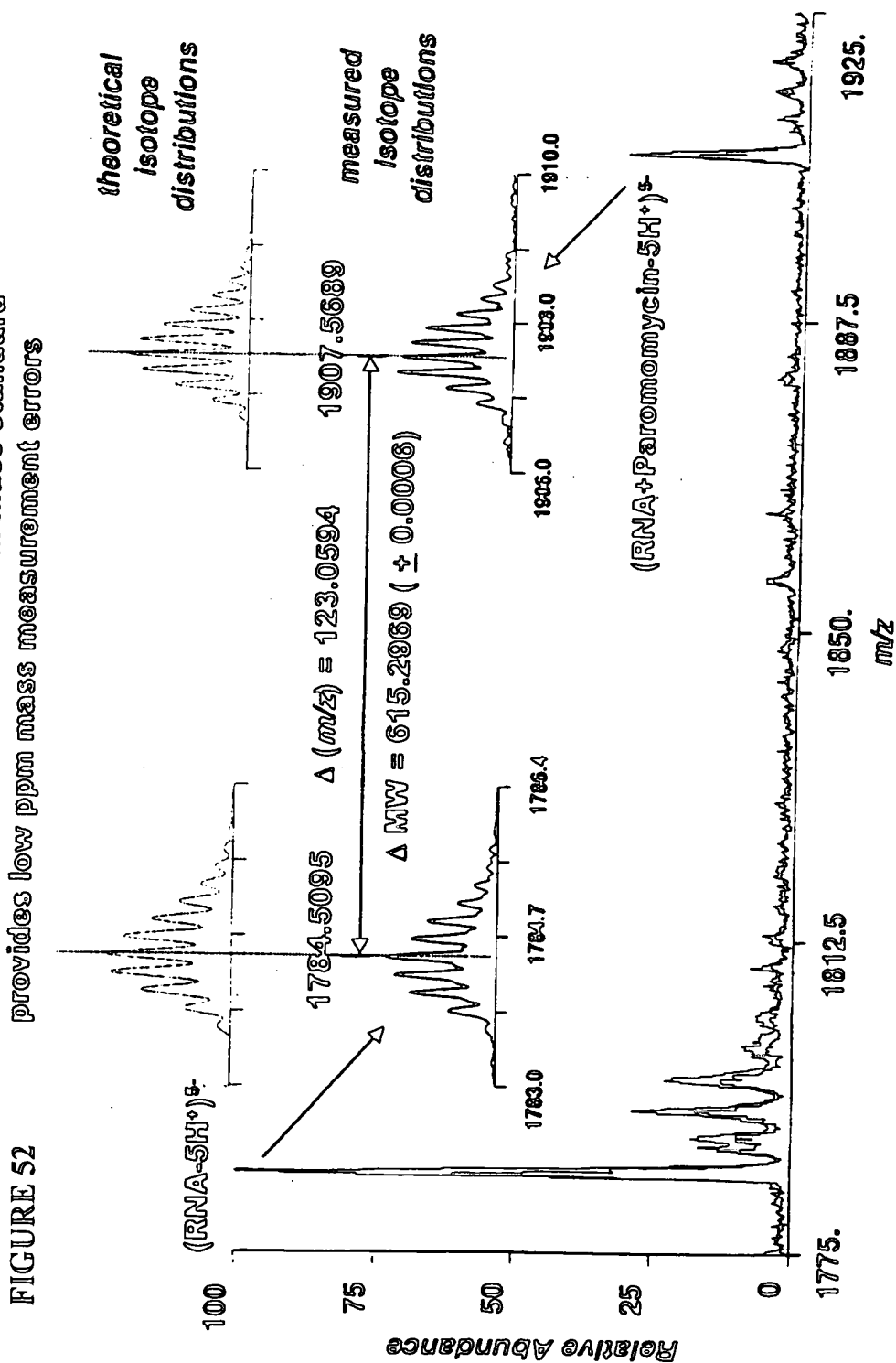


Figure 53

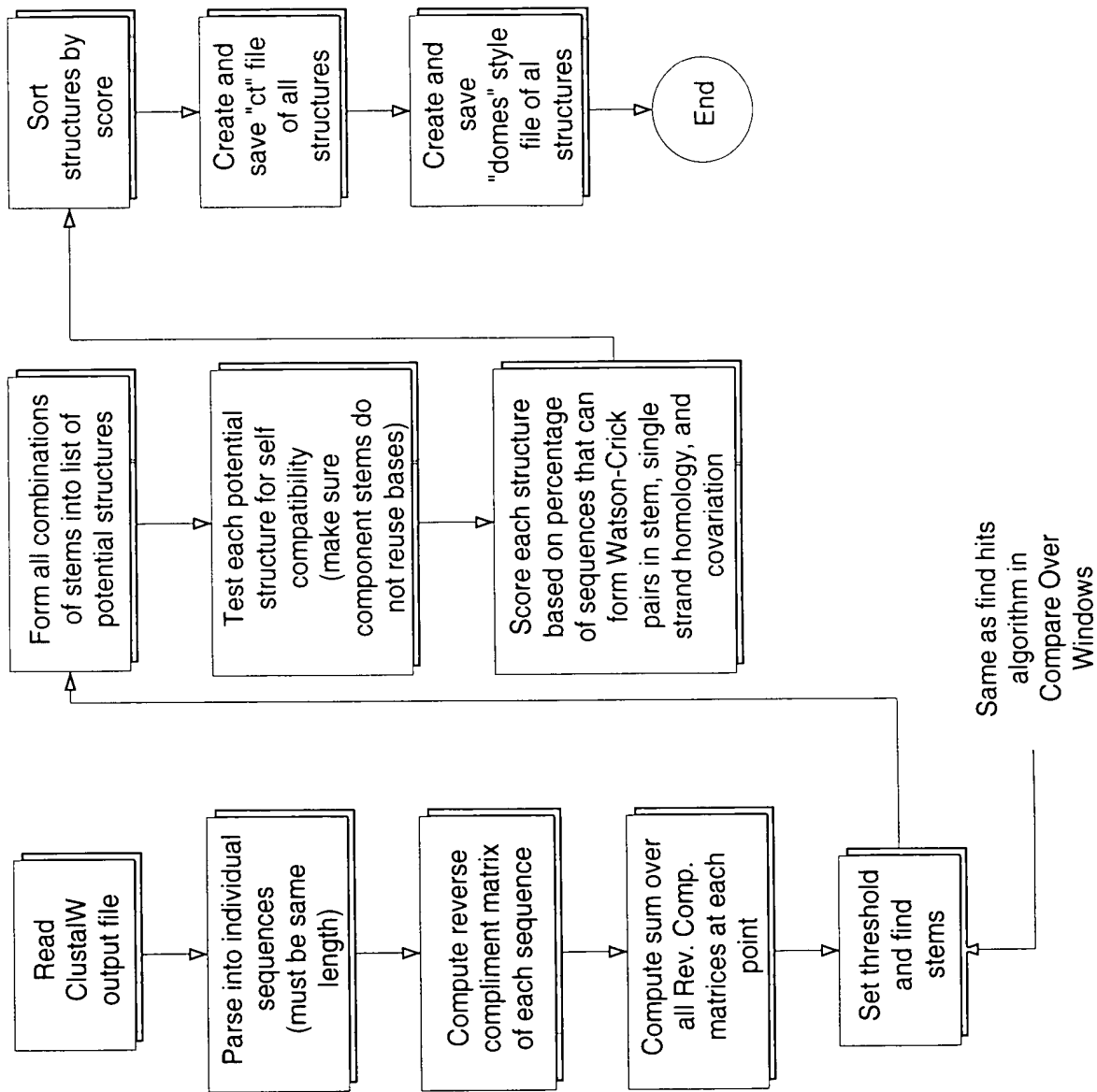
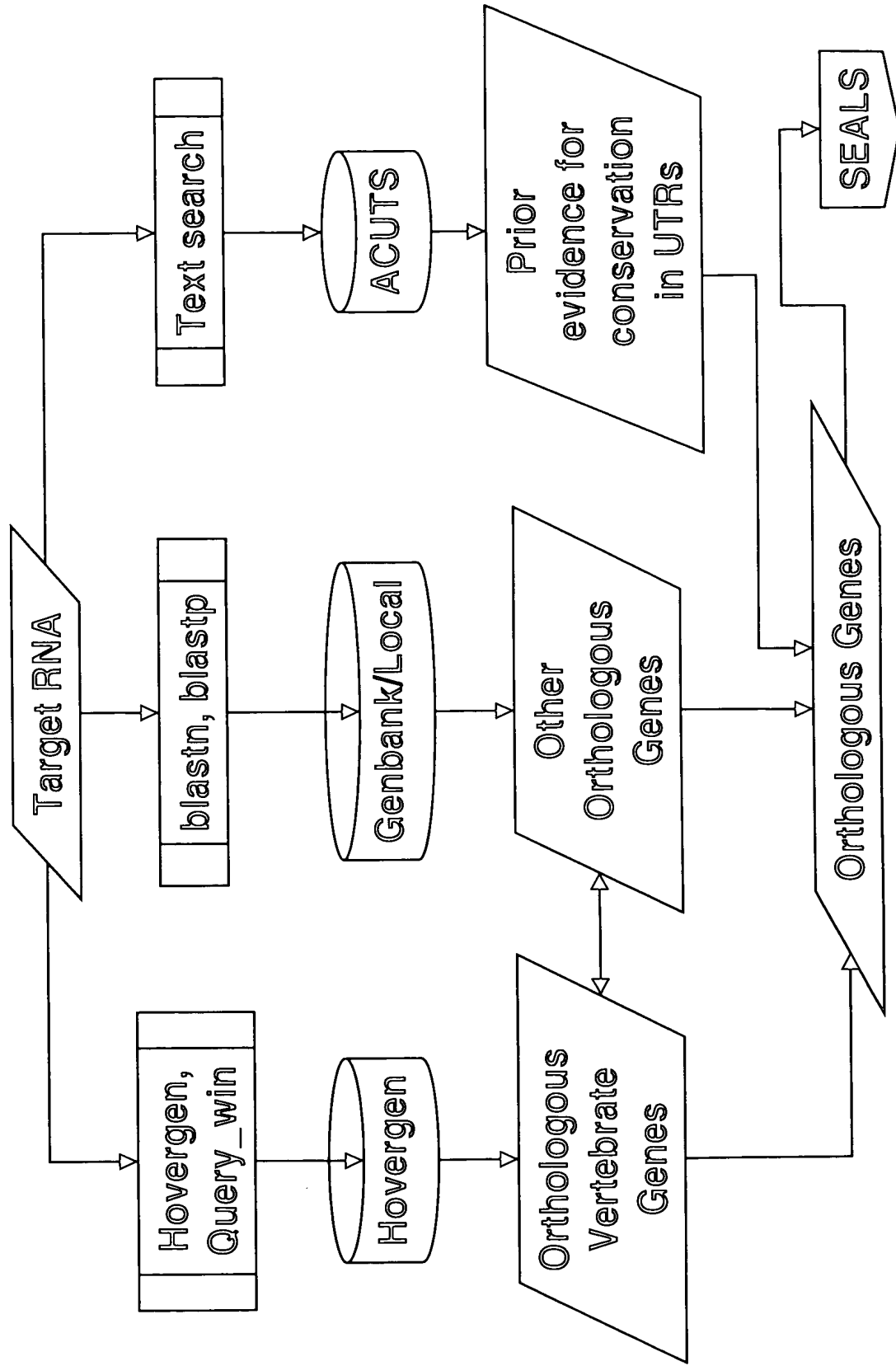


Figure 54



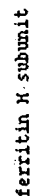
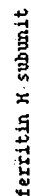
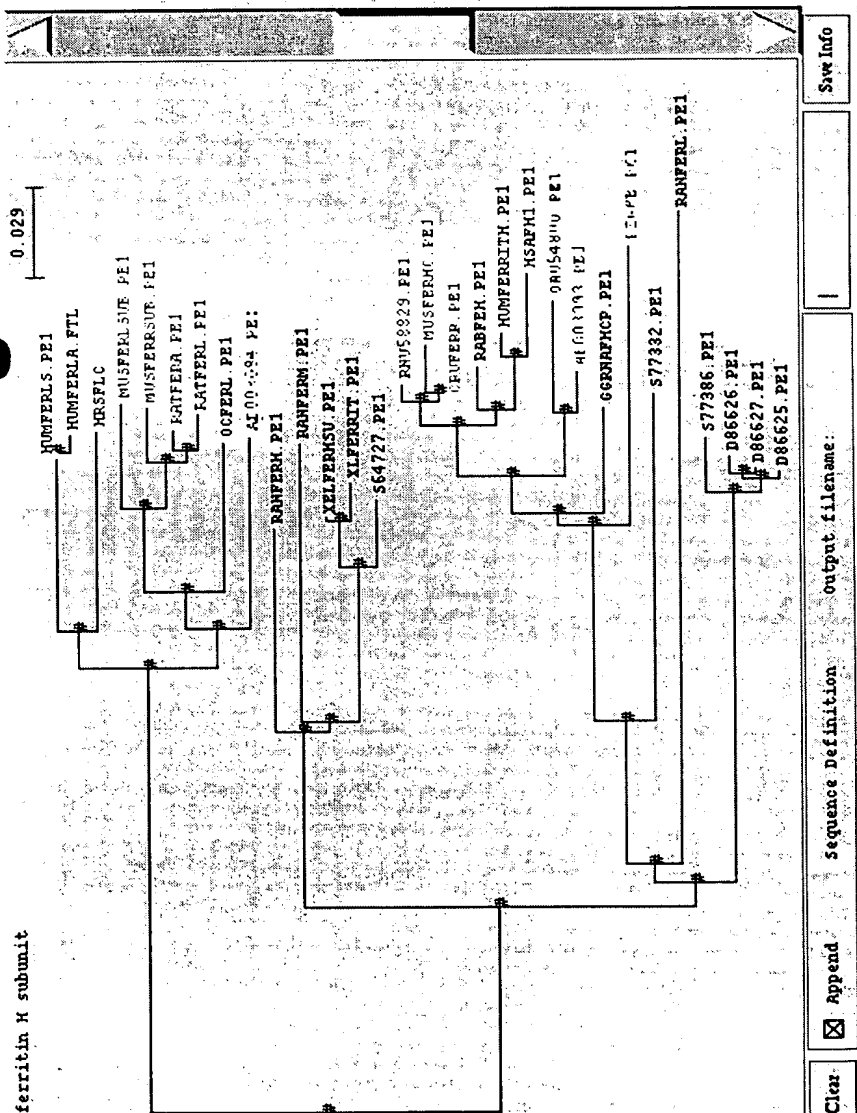


Figure 56






HOVERGEN <i>Homoilogous Vertebrate Genes Data Base</i>																											
Warning: Phylogenetic trees are unrooted! Select a gene or node (#) as outgroup to position the root (option= "New outgroup")																											
<input checked="" type="checkbox"/> Get info <input checked="" type="checkbox"/> Select for Alignment <input checked="" type="checkbox"/> Select for Output <input checked="" type="checkbox"/> New outgroup <input checked="" type="checkbox"/> Swap nodes <input checked="" type="checkbox"/> Sub - tree <input checked="" type="checkbox"/> Reset tree	<div style="margin-bottom: 10px;"> <input type="checkbox"/> Small leaf <input type="checkbox"/> Branch lengths </div> <div style="display: flex; justify-content: space-around;">   </div>																										
tree display ... miscellaneous ...																											
<div style="display: flex; justify-content: space-between;"> Legend for Taxon Color mammalian orders Apply </div> <div style="display: flex; align-items: center; margin-top: 10px;"> <div style="flex-grow: 1;"> Hovergen color file : _____ <div style="border: 1px solid black; padding: 2px; display: inline-block;">hovergen.color</div> </div> <div style="flex-grow: 1; text-align: right;"> Change Color Set  </div> </div>																											
<table border="1" style="width: 100%; border-collapse: collapse;"> <tbody> <tr><td><input type="checkbox"/></td><td>PRIMATES</td></tr> <tr><td><input type="checkbox"/></td><td>RODENTIA</td></tr> <tr><td><input type="checkbox"/></td><td>ARTIODACTYLA</td></tr> <tr><td><input type="checkbox"/></td><td>LAGOMORPHA</td></tr> <tr><td><input type="checkbox"/></td><td>CARNIVORA</td></tr> <tr><td><input type="checkbox"/></td><td>CETACEA</td></tr> <tr><td><input type="checkbox"/></td><td>PERISSODACTYLA</td></tr> <tr><td><input type="checkbox"/></td><td>CHIROPTERA</td></tr> <tr><td><input type="checkbox"/></td><td>INSECTIVORA</td></tr> <tr><td><input type="checkbox"/></td><td>MONOTREMATA</td></tr> <tr><td><input type="checkbox"/></td><td>EDENTATA</td></tr> <tr><td><input type="checkbox"/></td><td>MAMMALIA</td></tr> <tr><td><input type="checkbox"/></td><td>Other</td></tr> </tbody> </table> <div style="text-align: right; margin-top: 10px;"> <input type="checkbox"/> auto </div>		<input type="checkbox"/>	PRIMATES	<input type="checkbox"/>	RODENTIA	<input type="checkbox"/>	ARTIODACTYLA	<input type="checkbox"/>	LAGOMORPHA	<input type="checkbox"/>	CARNIVORA	<input type="checkbox"/>	CETACEA	<input type="checkbox"/>	PERISSODACTYLA	<input type="checkbox"/>	CHIROPTERA	<input type="checkbox"/>	INSECTIVORA	<input type="checkbox"/>	MONOTREMATA	<input type="checkbox"/>	EDENTATA	<input type="checkbox"/>	MAMMALIA	<input type="checkbox"/>	Other
<input type="checkbox"/>	PRIMATES																										
<input type="checkbox"/>	RODENTIA																										
<input type="checkbox"/>	ARTIODACTYLA																										
<input type="checkbox"/>	LAGOMORPHA																										
<input type="checkbox"/>	CARNIVORA																										
<input type="checkbox"/>	CETACEA																										
<input type="checkbox"/>	PERISSODACTYLA																										
<input type="checkbox"/>	CHIROPTERA																										
<input type="checkbox"/>	INSECTIVORA																										
<input type="checkbox"/>	MONOTREMATA																										
<input type="checkbox"/>	EDENTATA																										
<input type="checkbox"/>	MAMMALIA																										
<input type="checkbox"/>	Other																										

Figure 57

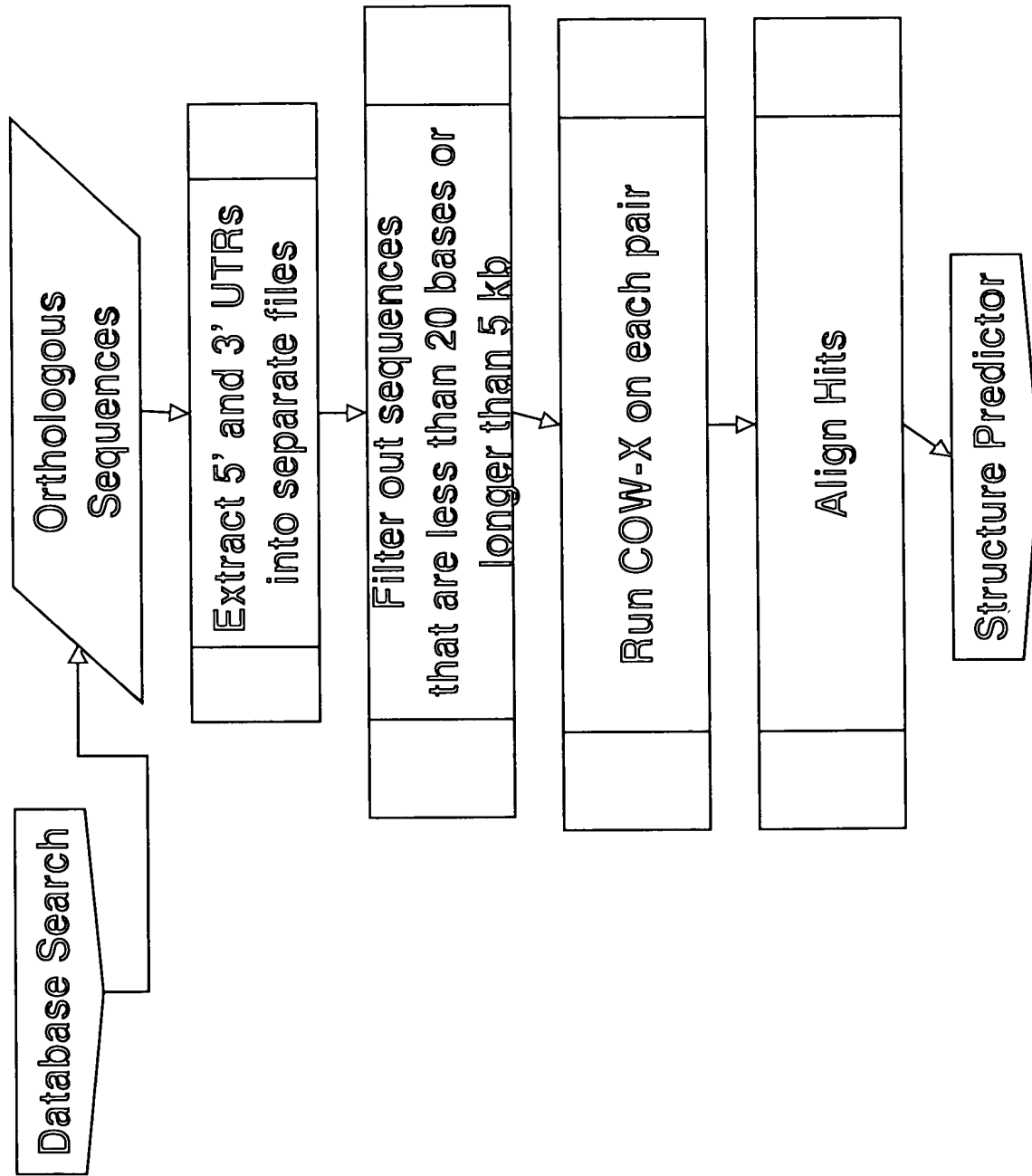


Figure 58

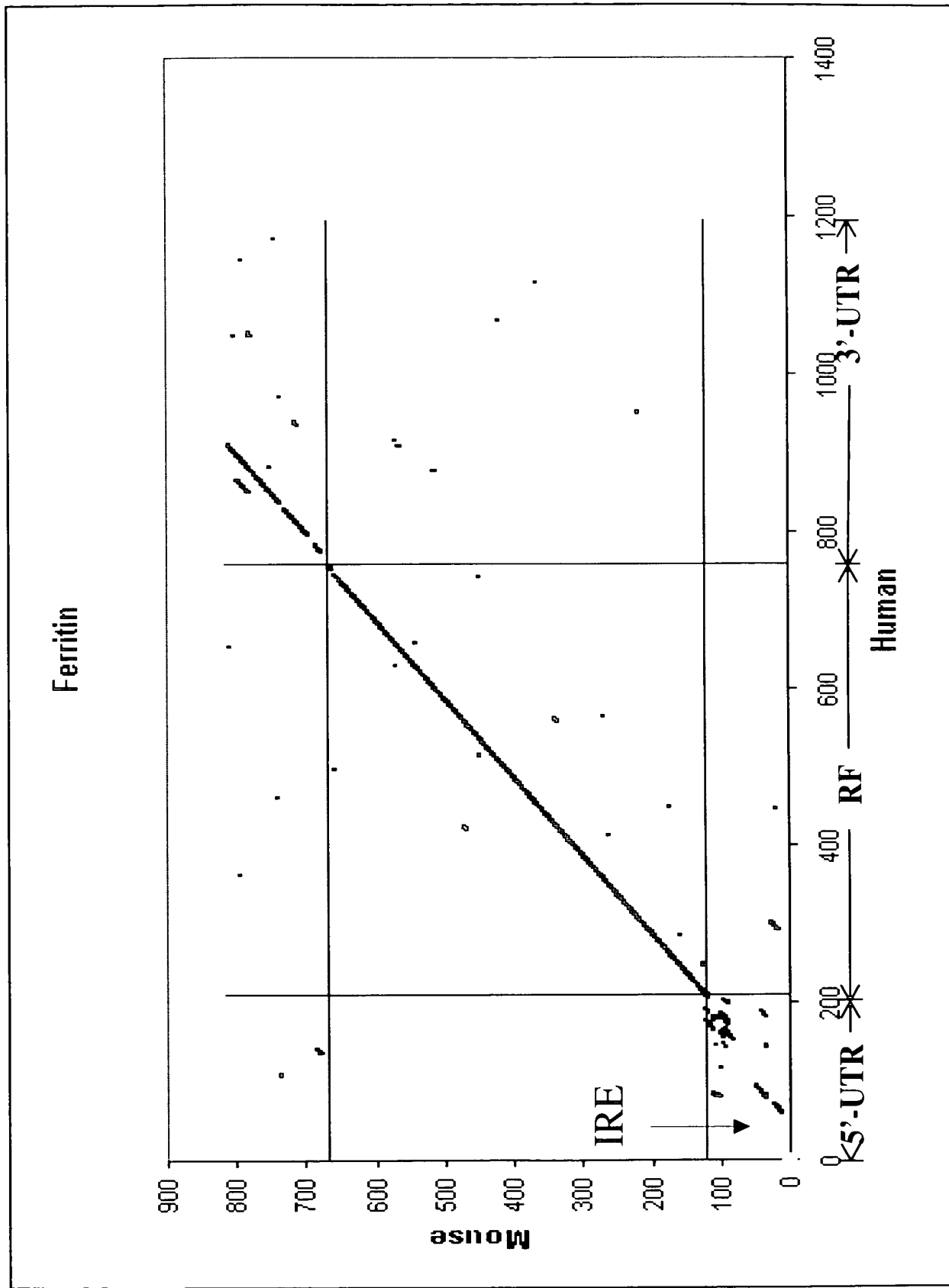
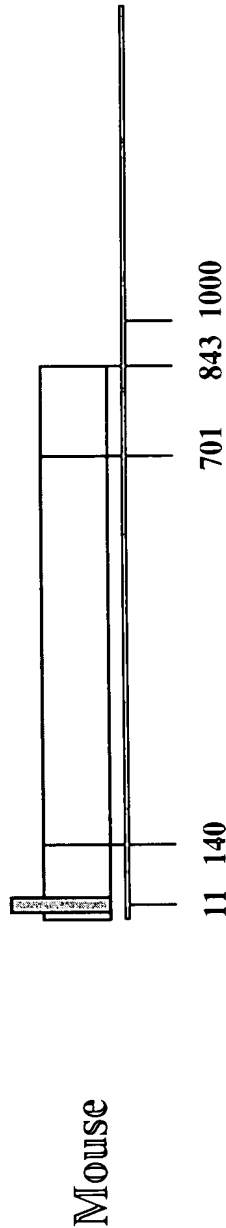
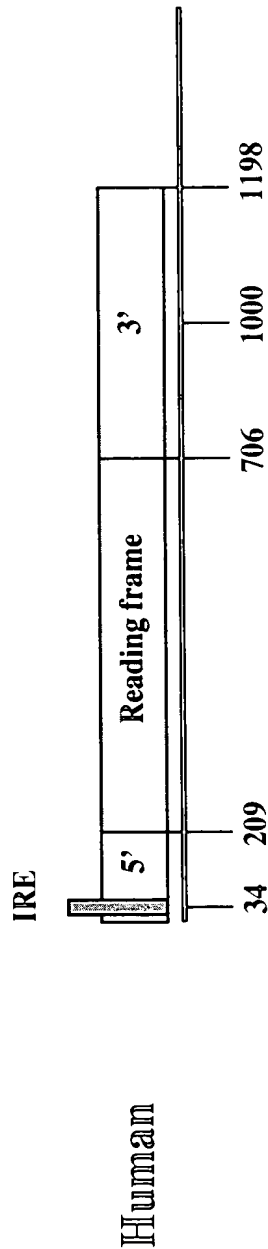


Figure 59



1000 900 800 700 600 500 400 300 200 100 0

Figure 60

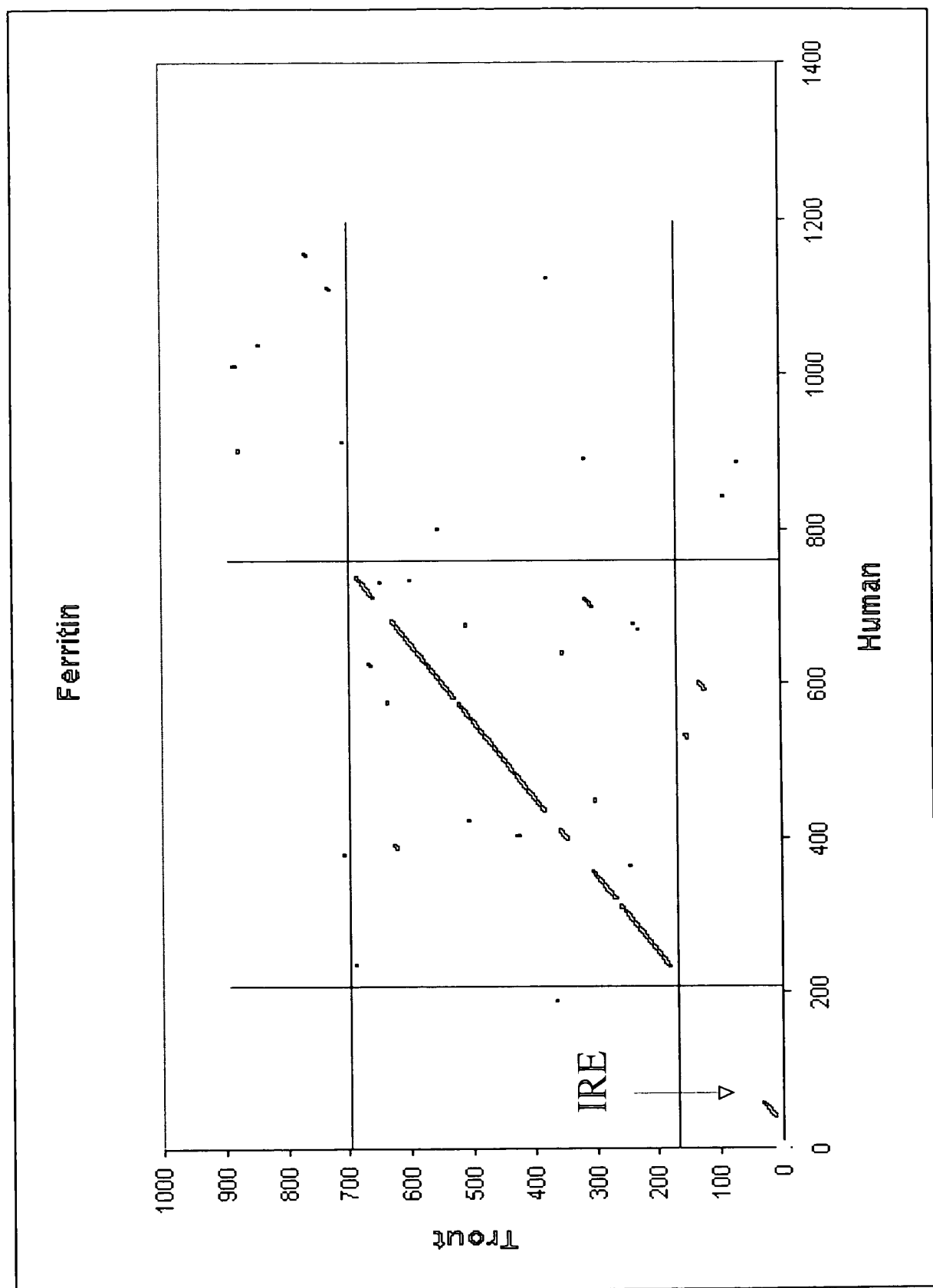


Figure 61

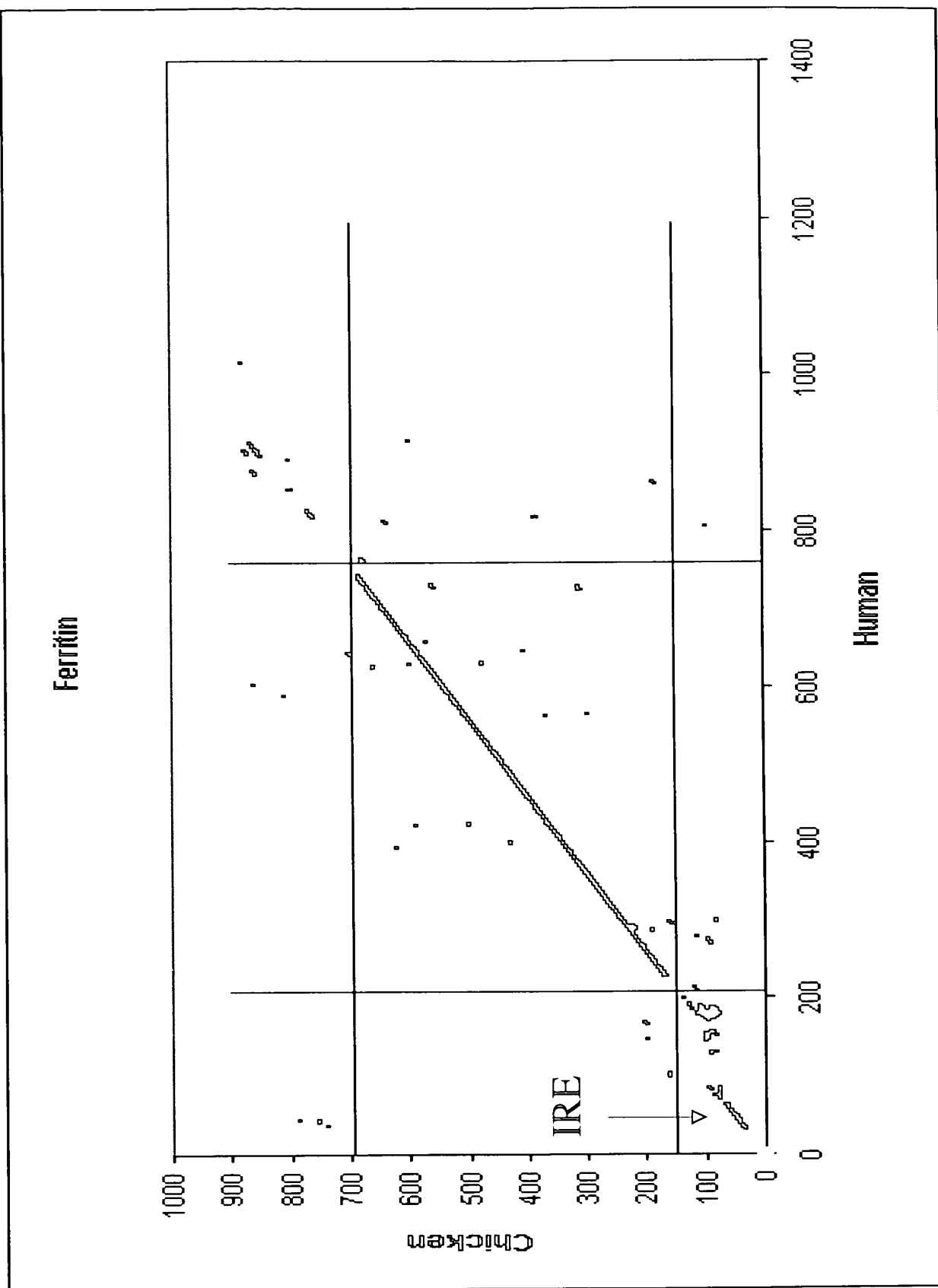


Figure 62

Conserved Region

t:507251cowx_0419:seqs5p									
Position:	Left Mean:	Left SD:	Right Mean:	Right SD:	Map directly to reference <input checked="" type="checkbox"/>				
Total hits:	Discard:	Net:	Start:	End:	Threshold: 1.0				
	Number	Description	Hits						
<input checked="" type="checkbox"/>	507251 fa	Homo sapiens 5 prime UTR							
<input type="checkbox"/>	2879899 fa	Bos taurus 5 prime UTR (ori...							
<input type="checkbox"/>	1305504 fa	Ovis aries 5 prime UTR (orig...							
<input type="checkbox"/>	286151 fa	Sus scrofa 5 prime UTR (ori...							
<input type="checkbox"/>	1435202 fa	Rattus norvegicus 5 prime U...							
<input type="checkbox"/>	191071 fa	Cricetulus griseus 5 prime U...							
<input type="checkbox"/>	2369860 fa	Gallus gallus 5 prime UTR (...							
<input type="checkbox"/>	999126 fa	Salmo salar 5 prime UTR (o...							
<input type="checkbox"/>	1752749 fa	Oncorhynchus mykiss 5 pri...							
<input type="checkbox"/>	213691 fa	Rana catesbeiana 5 prime U...							
<input checked="" type="checkbox"/>	238858 fa	Xenopus laevis 5 prime UTR							
<input type="checkbox"/>	2183236 fa	Asterias forbesii 5 prime UT...							
<input type="checkbox"/>	9649 fa	Lymnaea stagnalis 5 prime							
<input type="checkbox"/>	559066 fa	Aedes aegypti 5 prime UTR (...							
<input type="checkbox"/>	443646 fa	Drosophila melanogaster 5							
Hits on sequence 507251									
507251 fa	Start	End	Position	Length	Via	Alignment	Sequence		
>gl 507251 L20941	79	87	33	9	238858	-46	CTGCTTCAA		
Homo sapiens 5 prime UTR origin	261	270	35	10	238858	-226	GCTTCAACAG		
CAGAGTTCTTCGCCGAGAGTCGT	353	368	127	16	238858	-226	CGGACTGCCCAAGGC		
CGGGGTTCTCTGCTTCAACAGTCC	359	369	99	11	238858	-260	GCCCTCCGTC		
TTGGACGGAGACCGCGCTCGTTC	502	533	30	32	238858	-472	TTCTCTGCTTCACAATGCTTGGACGGAACCCG		
CCACCCCGCGCGCGCCGCTCA	524	534	117	11	238858	-407	ACCGCACCTC		
GCCAGCCCTCCCGTCACGCTTCA									

Figure 63

5p_xenopus_500_535_auto.aln [Read-Only]		A		E
1	CLUSTAL W (1.74) multiple sequence alignment			
2				
3				
4	gi 1752749 D86626	AGAAGTTGCTTCAACAGTGATTGAACGGAACTCCTC-		
5	gi 999126 S77386	AGTTCTTGCTTCAACAGTGATTGAACGGAACTCCTC-		
6	gi 213691 M12120	AGTTCTTGCTTCAACAGTGTTTGAACGGAAAC-CCTCT		
7	gi 238858 S64727	AGTTCTTGCTTCAACAGTGTTTGAACGGAAAC-CCTCT		
8	gi 286151 D15071	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGC-		
9	gi 507251 L20941	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGC-		
10	gi 191071 W99692	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGC-		
11	gi 2369860 Y14698	GTTTCCTGCTTCAACAGTGCTTGGACGGAAACCCGGCC-		
12		*** ***** *	***** *	*
13				
14				
15				

Figure 64

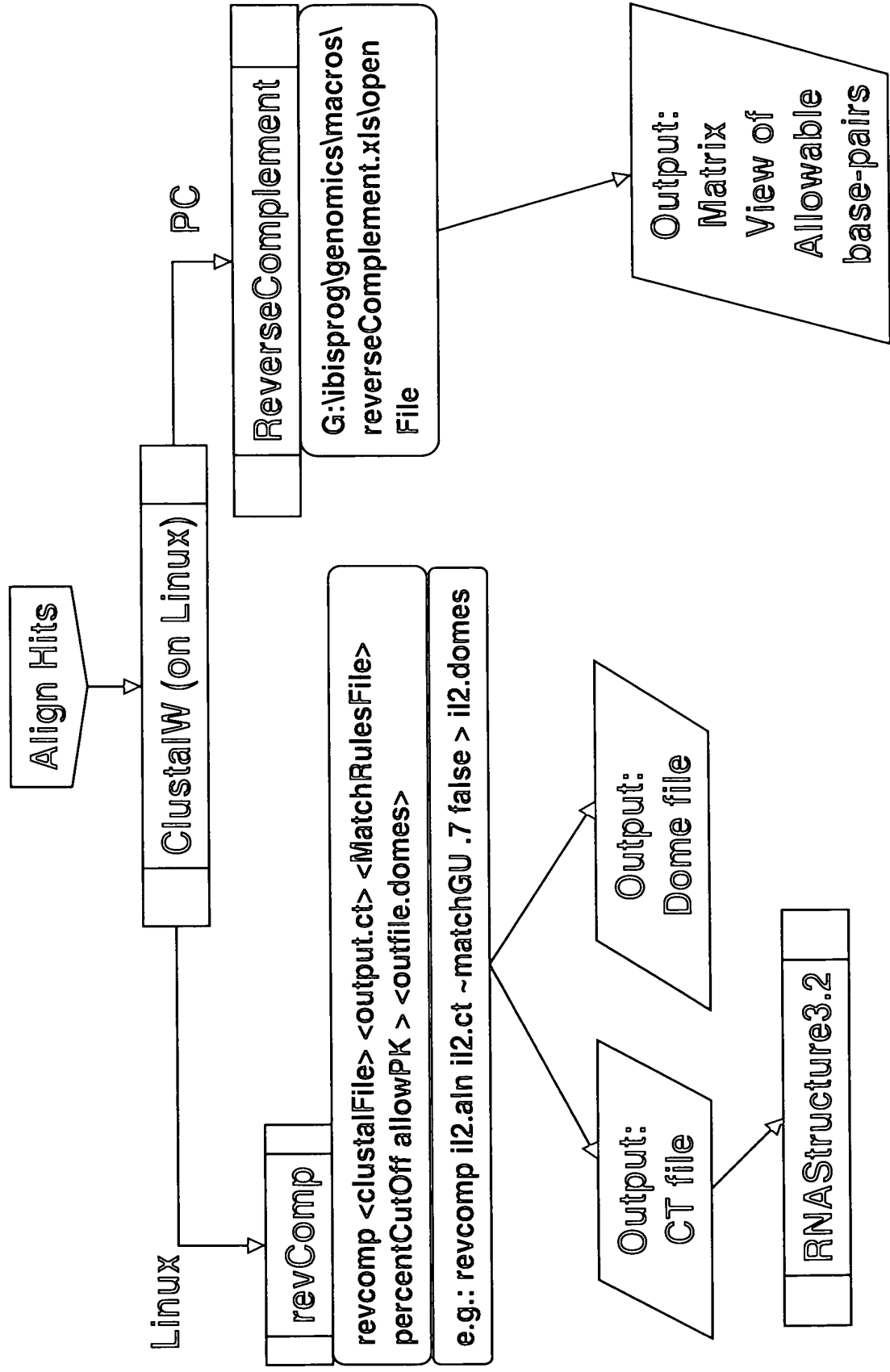


Figure 65

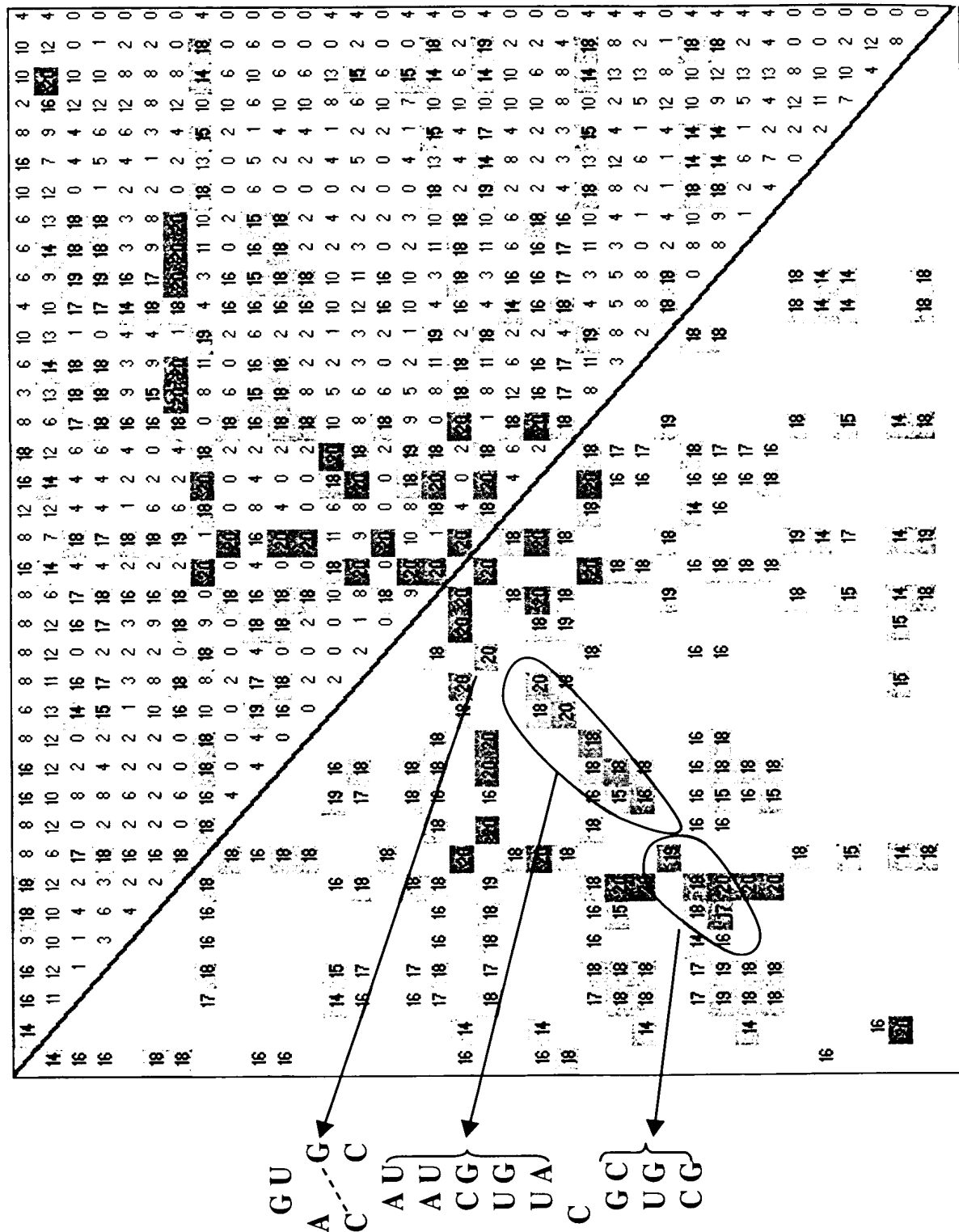


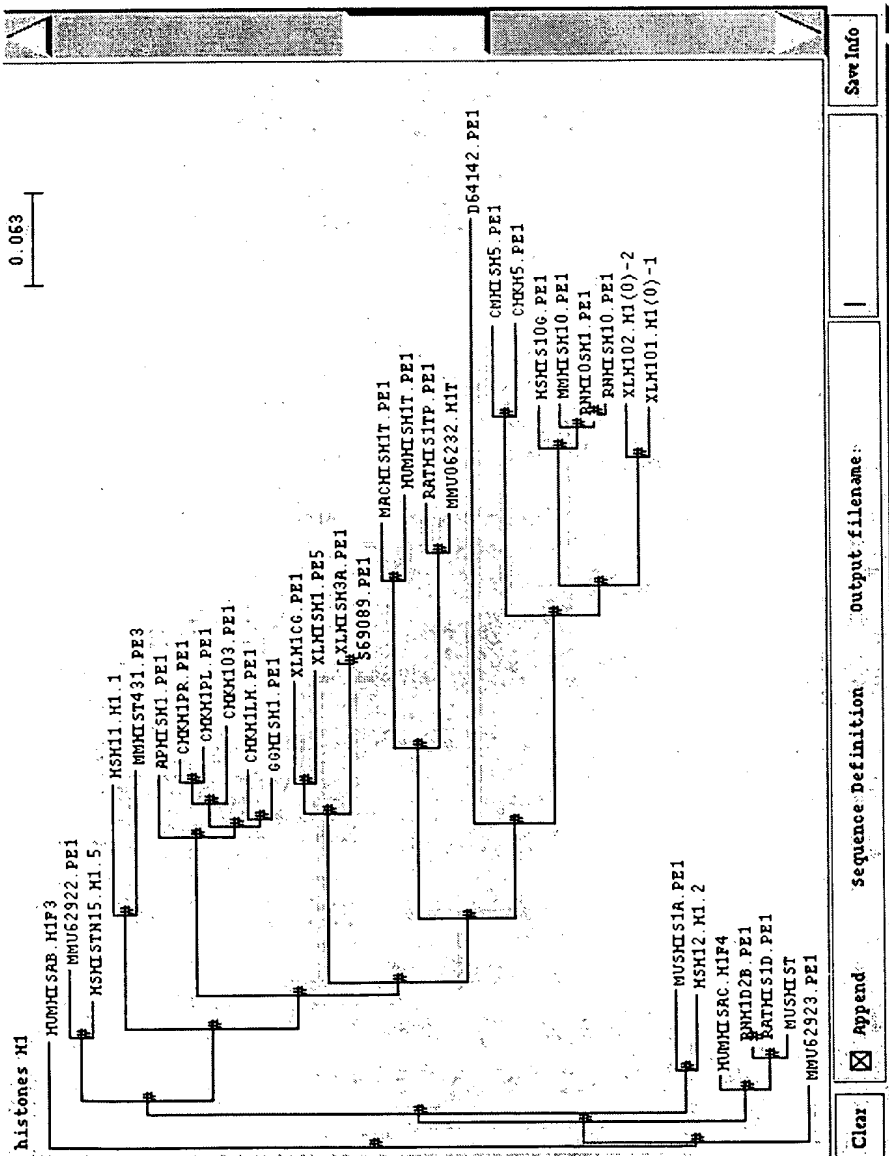
Figure 67

IRE Structures for each species

<p>G-U A G C C</p> <p>A-U A-U C-G U-G U-A</p> <p>C G-C U-G C-G</p> <p>HUMAN PIG</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-A U-A</p> <p>C G-C U-G C-G</p> <p>HAMSTER MOUSE RAT</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-G G-A</p> <p>C G-C U-G C-G</p> <p>CHICKEN</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-A U-A</p> <p>C G-C U-G U-G</p> <p>TROUT SALMON</p>	<p>G-U A G C C</p> <p>A-U A-U C-G U-A U-A</p> <p>C G-C U-G U-G</p> <p>XENOPUS FROG</p>	<p>G-U A G C C</p> <p>C-G G-U C-G G-U U-A</p> <p>C U-A U-A C-G</p> <p>FLY</p>	<p>G-U A G C C</p> <p>C-G G-U C-G G-U U-A</p> <p>C U-A U-A C-G</p> <p>MOSQUITO</p>
---	---	---	--	--	---	--

[illegible]

Figure 69



HOVERGEN homologous Vertebrate Genes Data Base

Warning: Phylogenetic trees are unrooted!
Select a gene or node (#) as outgroup to position the root (option= 'New outgroup')

- ☒ Get info
- ☒ Select for Alignment
- ☒ Select for Output
- ☒ New outgroup
- ☒ Swap nodes
- ☒ Sub-tree
- ☒ Reset tree

☐ Small leaf

☐ Branch lengths

tree display ... miscellaneous ...

☒ New Tree

Legend for Taxon Color

vertebrate classes

Apply

Howzgen color file

Change Color Set

howzgen color

MAMMALIA

AVES

SAUROPSIDA

AMPHIBIA

LOBE-FINNED FISH AND TETRAPOD CLADE

ACTINOPTERYGII

CHONDRICTHYES

PETROMYZONTIFORMES

MYXINIFORMES

Other

Save Info

Sequence Definition

Output filename:

Append

Clear

Figure 70

Conserved Region

I:\HISTONE\cowx_0416\seqs3p

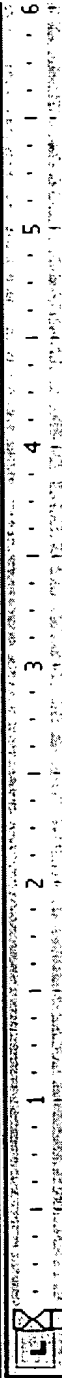
Position:		Left Mean:		Left SD:	
Total hits:		Discarded:		Net:	
	Number	Description	Hits		
<input type="checkbox"/>	63477.fa	Gallus gallus 3 prime UTR [...]			
<input type="checkbox"/>	9788.fa	Pisaster brevispinus 3 prime...			
<input type="checkbox"/>	349586.fa	Volvox carteri 3 prime UTR [...]			
<input type="checkbox"/>	10044.fa	Pisaster ochraceus 3 prime ...			
<input type="checkbox"/>	9989.fa	Pycnopodia helianthoides 3 ...			
<input checked="" type="checkbox"/>	161381.fa	Psammochinus miliaris 3 pr...			
<input type="checkbox"/>	9614.fa	Lytechinus pictus 3 prime U...			
<input type="checkbox"/>	31967.fa	Homo sapiens 3 prime UTR ...			
<input type="checkbox"/>	64766.fa	Xenopus laevis 3 prime UTR...			
<input type="checkbox"/>	404465.fa	Styela plicata 3 prime UTR [...]			
<input type="checkbox"/>	342113.fa	Macaca mulatta 3 prime UT...			
<input type="checkbox"/>	797284.fa	Paracentrotus lividus 3 prim...			
<input type="checkbox"/>	287651.fa	Rattus norvegicus 3 prime U...			
<input type="checkbox"/>	2292939.fa	Mus musculus 3 prime UTR ...			
<input type="checkbox"/>	62730.fa	Cairina moschata 3 prime U...			
<input type="checkbox"/>	10251.fa	Strongylocentrotus purpuratu...			
<input type="checkbox"/>	62440.fa	Anas platyrhynchos 3 prime ...			
<input type="checkbox"/>	10338.fa	Solaster stimpsoni 3 prime ...			
<input type="checkbox"/>	515003.fa	Mus pahari 3 prime UTR [ori...			

Figure 71

3p_xenopus_23_56_auto.aln [Read-Only]		A	
1	CLUSTAL W (1.74) multiple sequence alignment		
2			
3			
4	gi 10044 X54113	-TAAACAAAACGGCTCTTTTCAGAGCCACCACTTC-	
5	gi 9788 X54112	-TAAACAAAACGGCTCTTTTCAGAGCCACCACTTC-	
6	gi 9989 X54114	-TAATCAAAAACGGCTCTTTTCAGAGCCACCACTTC-	
7	gi 10251 V01356	ATACACAAA-CGGCTCTTTTCAGAGCCACCACAAC-	
8	gi 161381 M10558	ATACACAAA-CGGCTCTTTTCAGAGCCACCACAAC-	
9	gi 9614 X00628	TAACCAAAA-CGGCTCTTTTCAGAGCCACCAATAAC-	
10	gi 404465 S64499	-GACACAAAACGGCTCTTTTCAGAGCCACCA-ATCG	
11	gi 31967 X57129	AAACCCA-AAAGGCTCTTTTCAGAGCCACCACTGA-	
12	gi 515003 X80327	-CCCCACAAAGGCTCTTTTCAGAGCCACCACTGC-	
13	gi 2292939 Y12291	-CAATCCAAAAGGCTCTTTTCAGAGCCACCACTCC-	
14	gi 287651 X67320	-ACAACCCAAAGGCTCTTTTCAGAGCCACCCACAA-	
15	gi 342113 M97756	-AGAACCCAAAGGCTCTTTTAAGAGCCACCCACAT-	
16	gi 63477 X01752	-GATATCCAAAGGCTCTTTTAAGAGCCACCCACAC-	
17	gi 64766 X03017	-TATACCCAAAGGCTCTTTTCAGAGCCACCCACCC-	
18	gi 62440 X06128	-TAAACCCAAAGGCTCTTTTAAGAGCCACCCACTT-	
19	gi 62730 X14731	-TTAACCCAAAGGCTCTTTTCAGAGCCACCAACTT-	
20	gi 10338 X54115	-CAAAACCGAACGGCCCTTTTAGGCCACTACACTTT-	
21		* * * * *	* * *
22		NNNNNNNNANNGGCNCTTTTNNNNNNNNNNNNNNNN	
23			

Figure 73

histone.domes (Read-Only)



NNNNNNNNANNGGCNCUUUUNNGNNNCNNNNNNNN	Consensus
-UAAACAAAACGGCUCUUUUCAGAGCCACCACUUC-	gi 10044 X54113
-UAAACAAAACGGCUCUUUUCAGAGCCACCACUUC-	gi 9788 X54112
-UAAUCAAAACGGCUCUUUUCAGAGCCACCACUUC-	gi 9989 X54114
AUACACAAA-CCGGCUCUUUUCAGAGCCACCACAA-	gi 10251 V01356
AUACACAAA-CCGGCUCUUUUCAGAGCCACCACAA-	gi 161381 M10558
UAACCAAAA-CCGGCUCUUUUCAGAGCCACCACAA-	gi 9614 X00628
-GACACAAAACGGCUCUUUUCAGAGCCACCACUUG	gi 404465 S64499
AAACCCA-AAAGGCUCUUUUCAGAGCCACCACUGA-	gi 31967 X57129
-CCCCACAAAAGGCUCUUUUCAGAGCCACCACUGC-	gi 515003 X80327
-CAAUCCAAAAGGCUCUUUUCAGAGCCACCACUCC-	gi 2292939 Y12291
-ACAACCCAAAAGGCUCUUUUCAGAGCCACCACAAA-	gi 287651 X67320
-AGAACCCAAAAGGCUCUUUUAAGAGCCACCACAU-	gi 342113 M97756
-GAUAUCCAAAGGCUCUUUUAAGAGCCACCACAC-	gi 63477 X01752
-UAUACCCAAAGGCUCUUUUCAGAGCCACCACCCC-	gi 64766 X03017
-UAAACCCAAAGGCUCUUUUAAGAGCCACCACUU-	gi 62440 X06128
-UUAACCCAAAGGCUCUUUUCAGAGCCACCACUU-	gi 62730 X14731
-CAAAACCGAACGGCCCCUUUUAAGGCCACUACACUU-	gi 10338 X54115

Figure 74

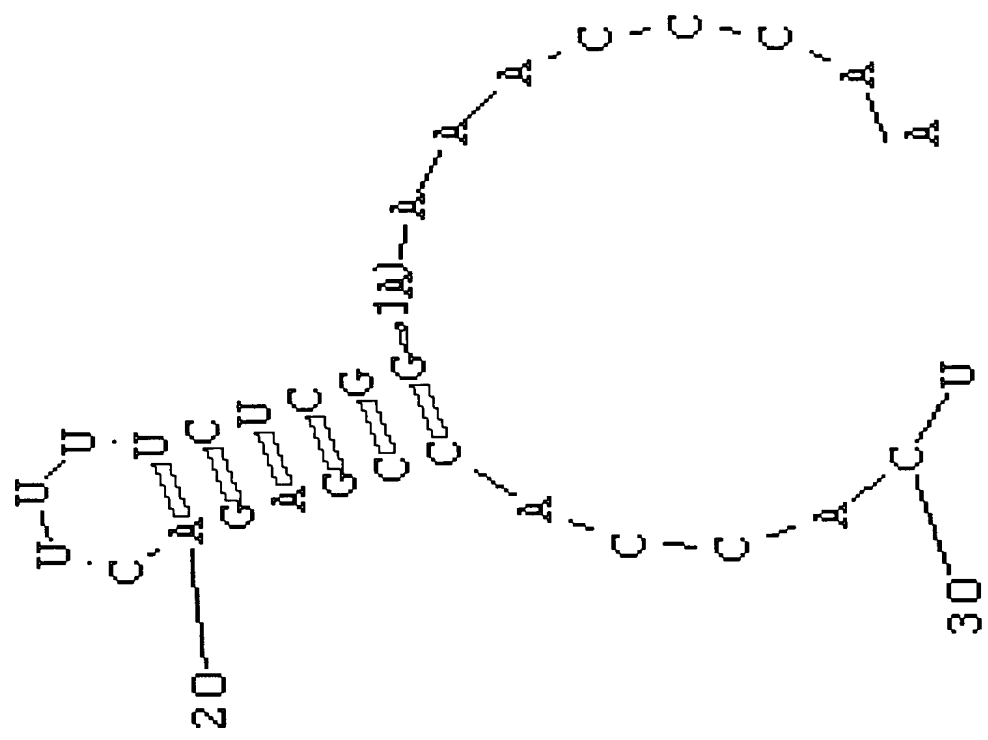


Figure 75

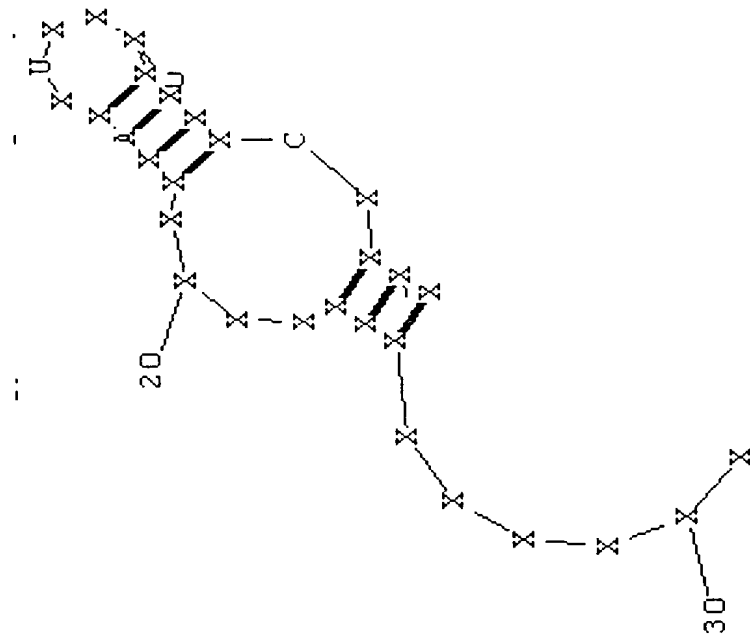


Figure 77

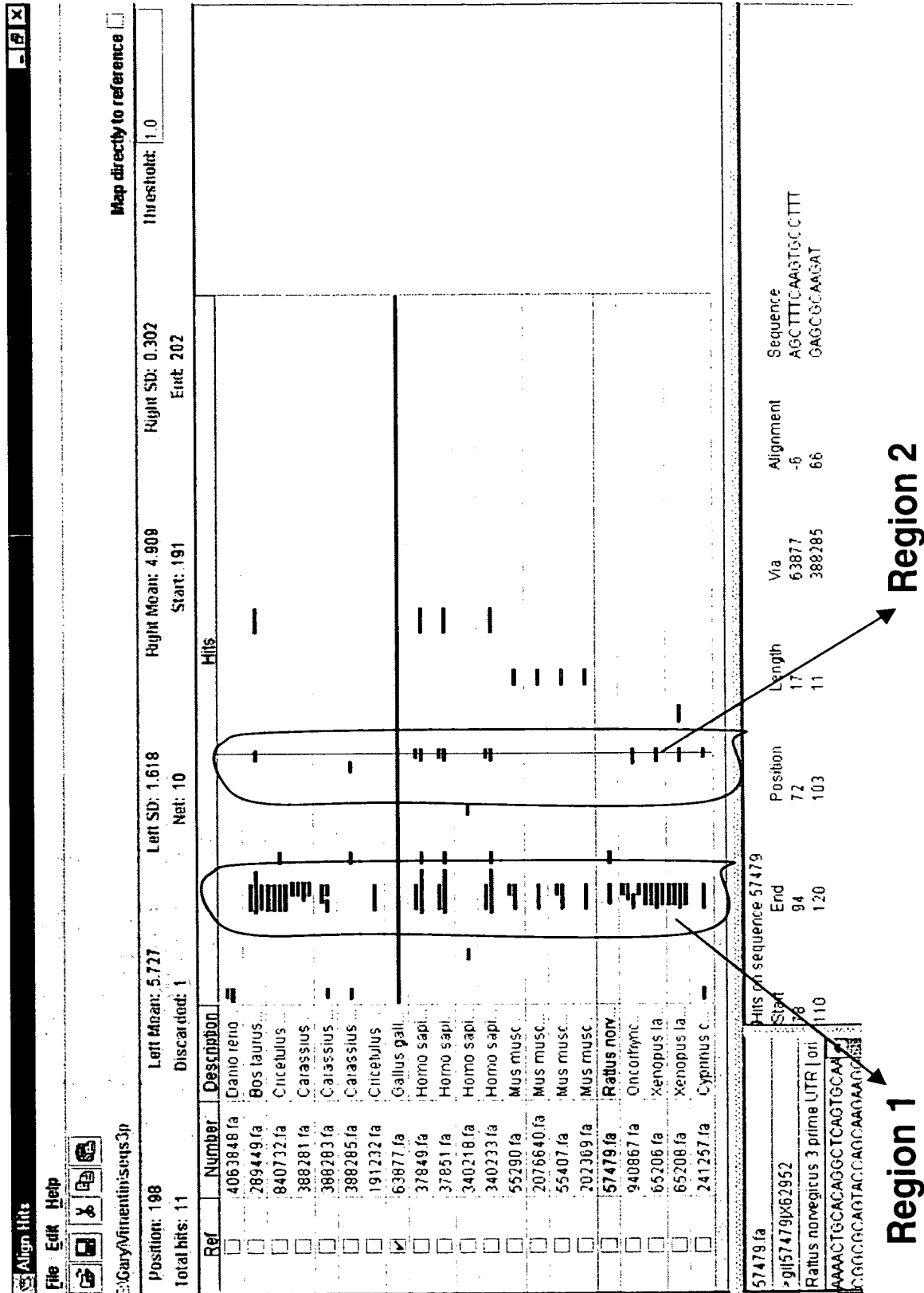
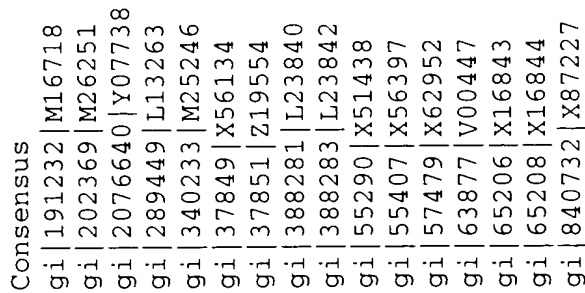


Figure 78

CLUSTAL W (1.74) multiple sequence alignment

```
gi|191232|M16718      TATCTTAAGGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGTAA
gi|202369|M26251      TATCTTAGGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
gi|2076640|Y07738     TATCTTAGGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
gi|289449|L13263      TATCTTAAAGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCG-AAGATA
gi|340233|M25246      TATCTTAAAGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
gi|37849|X56134       TATCTTAAAGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
gi|37851|Z19554       TATCTTAAAGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
gi|388281|L23840      CAACCCACAAATAACTGCTTCAAAGTGCCTTTC TGCACAGAAATA--GCCTTTGAGC
gi|388283|L23842      CTACCCACAAATAACTGCTTCAAAGTGCCTTTC TGC-CAGAAGTACAAAGCATTTGAGC
gi|55290|X51438       TATCTTAGGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
gi|55407|X56397       TATCTTAGGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
gi|57479|X62952       TATCTTAGAAATAAAAGCTTTC AAGTGCCTTTC TGCAGT TTT-CAGGAGCGCAAGATA
gi|63877|V00447       TGTCTTAAAGGAAGAGCTTTC AAGTGCCTTTC TCCAGT TTTTCATGAGCGCAAGATT
gi|65206|X16843       ACTTTGAAGAAACAGCTTTC AAGTGCCTTTT-TGCAGTCAATGGAGAGCGCAAGATA
gi|65208|X16844       AATTTGAAGAAACAGCTTTC AAGTGCCTTTT-TGCAGTTAATGGAGAGCGCAAGATA
gi|840732|X87227      TATCTTAAAGGAAACAGCTTTC AAGTGCCTTTC TGCAGT TTTTCAGGAGCGCAAGATA
```

Score: 445.0



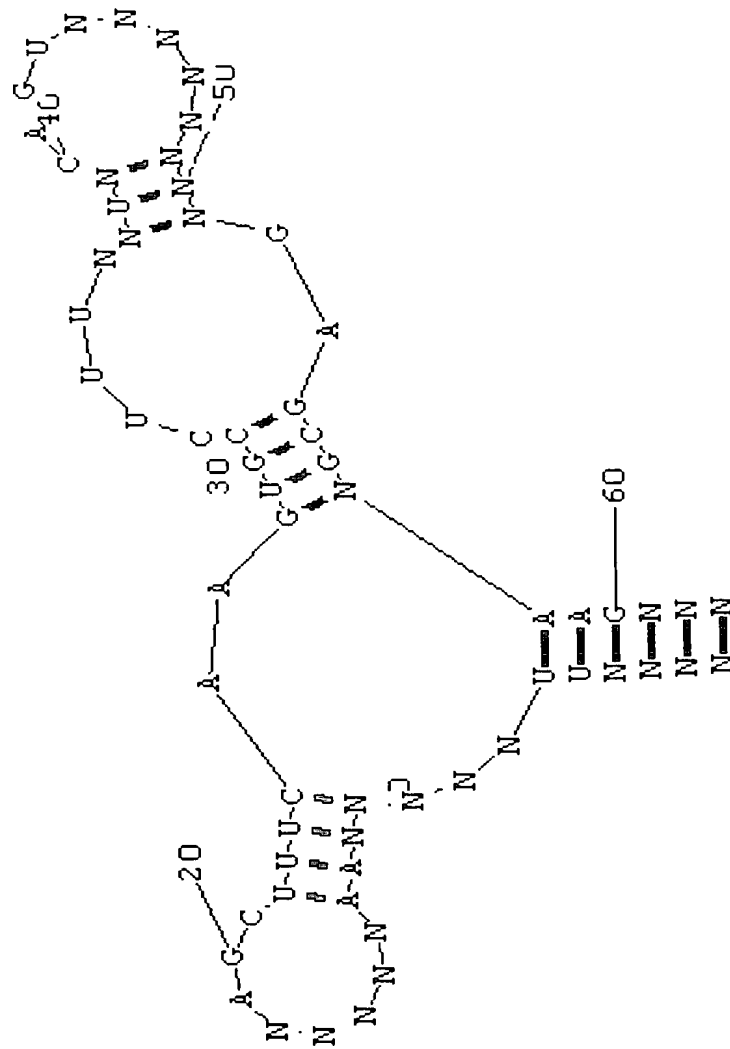


Figure 80

Figure 81

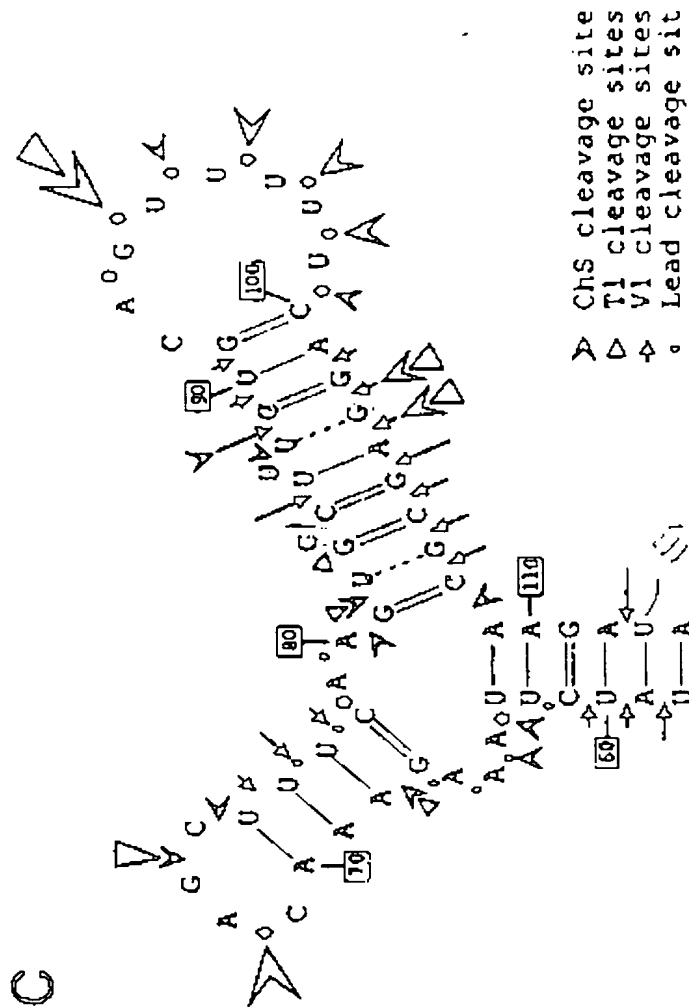


Figure 82

CLUSTAL W (1.74) multiple sequence alignment

gi 241257 S76850	ACCACGATGT-CTGTAGTTTACACTGTTGAA
gi 289449 L13263	TTTACAACATAATCTAGTTTACCGAAGACGC
gi 340233 M25246	TTTACAACATAATCTAGTTTACAGAAAATC
gi 37849 X56134	TTTACAACATAATCTAGTTTACAGAAAATC
gi 37851 Z19554	TTTACAACATAATCTAGTTTACAGAAAATC
gi 388285 L23841	TCCACACTGGAGTAAACGAGGAAGAATGAA
gi 63877 V00447	TTTACAATGGAGTCTAGTTTACAAATAGCAA
gi 65206 X16843	GCTTCCTTCT-GTCTAGTTTACAGACTGTAA
gi 65208 X16844	GCTTCCTTCT-GTCTAGTTTACAGACTATGT
gi 940867 Z50738	ACCACACTGA-GTCTAGTTTACACTTGGCT

Figure 84

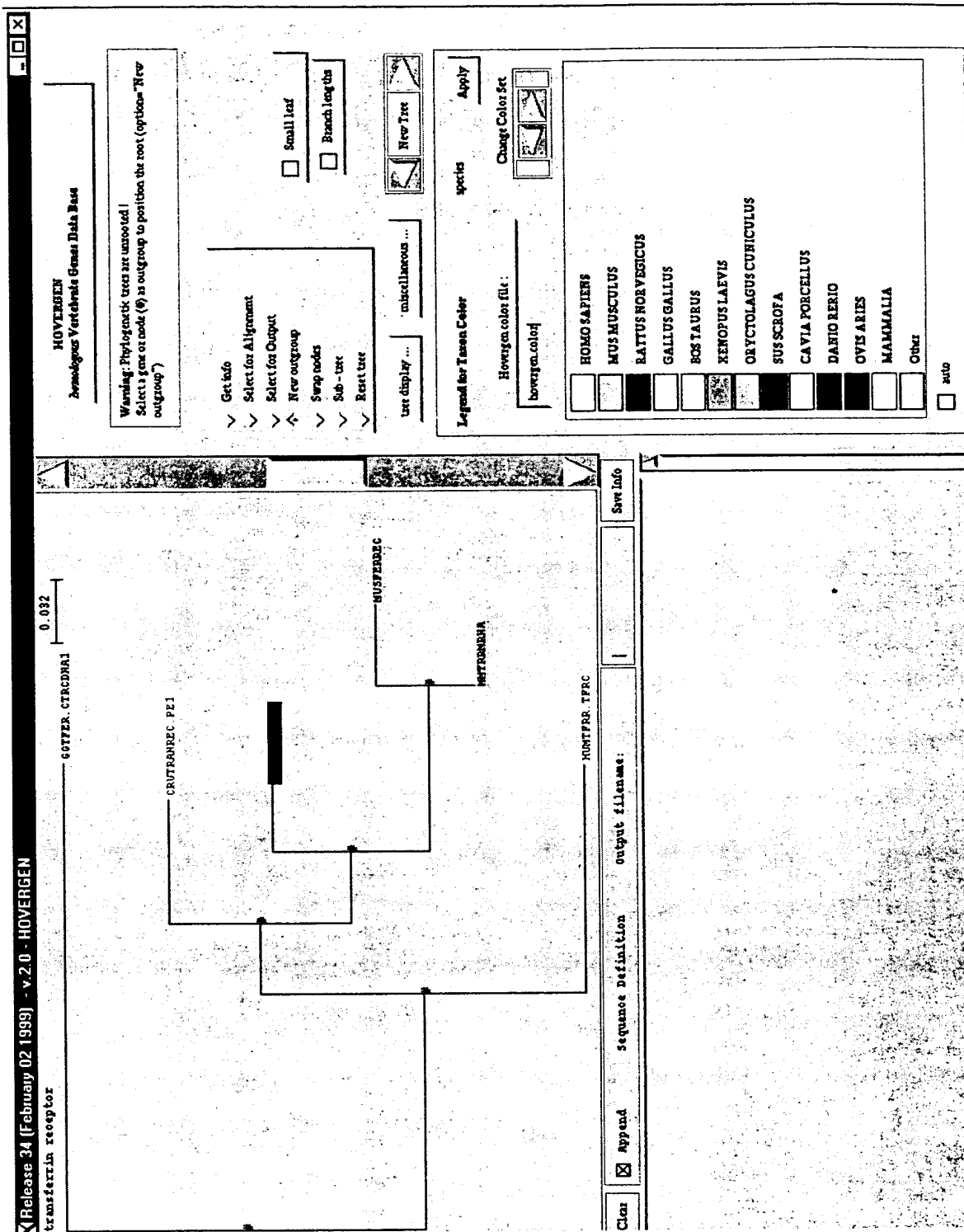


Figure 85

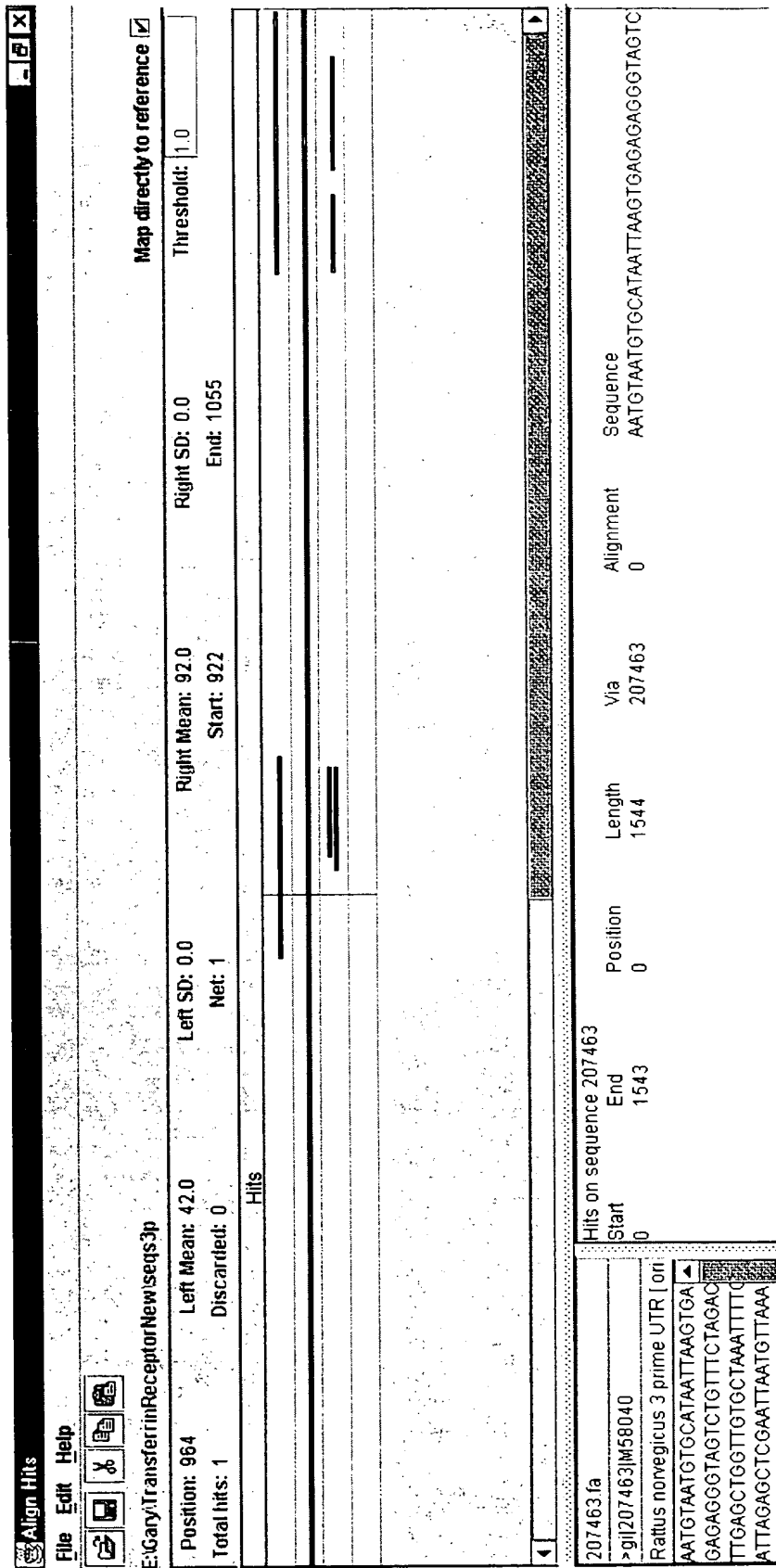


Figure 86

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
GTTTGTGGCACTGAGATATTTATTGTTTATTATCAGTGACAGAGTTCACATAAAATAGTGTTTTAAAT
gi|37432|X01060
CCTTTGGCACTGAGATATTTATTGTTTATTATCAGTGACAGAGTTCACATAAAATGGTGTTTTAAAT
gi|63357|X13753
-----
TGAGATATTTATTTTATTATCAGTGACAGCGTTCACATAAAATGGTGTTTTAT
```

Figure 87

Score: 102.0

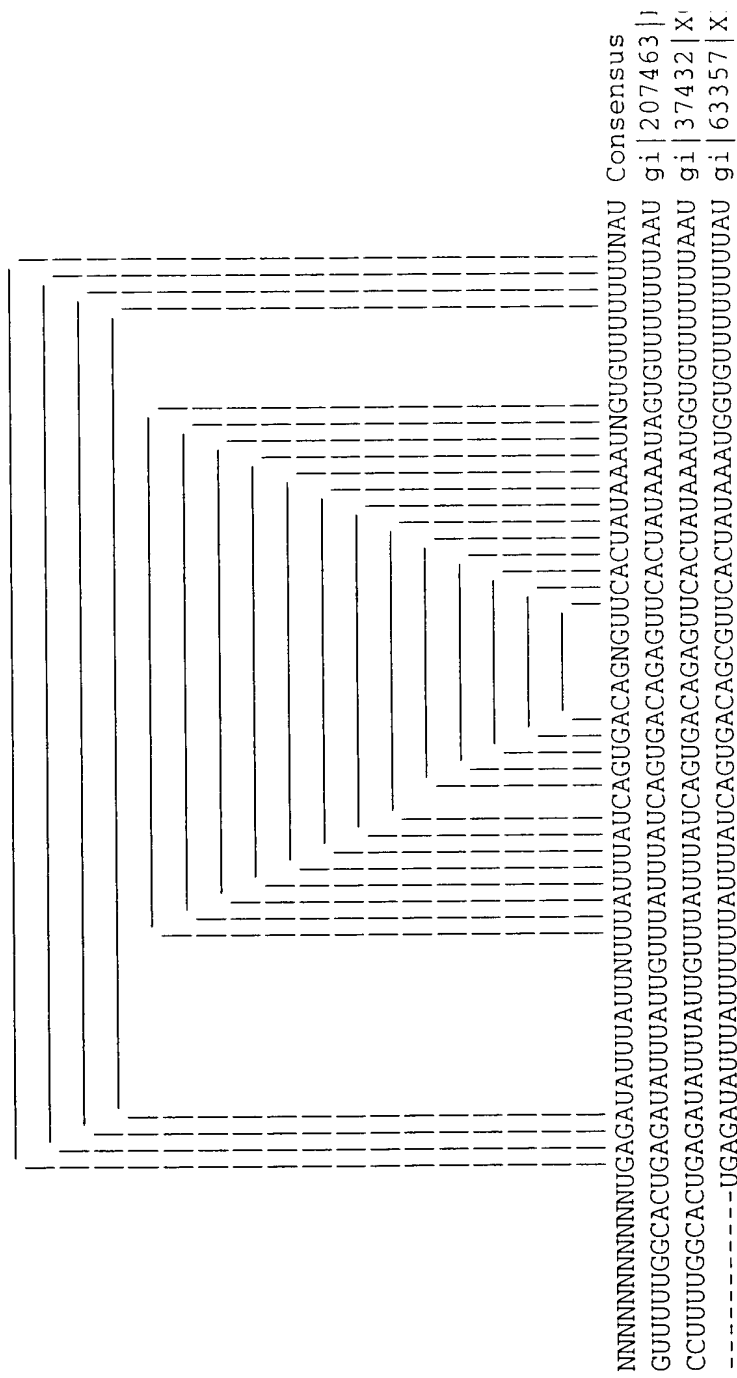
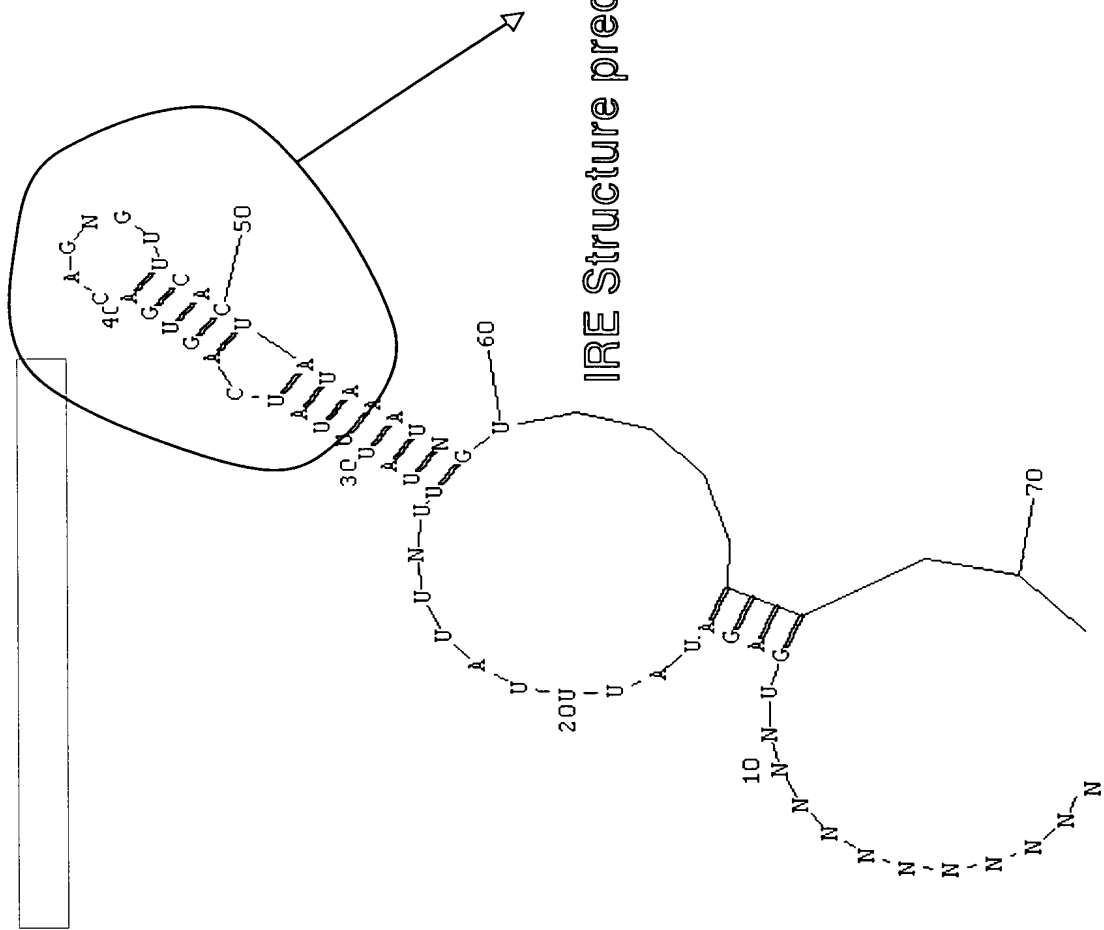


Figure 88



IRE Structure predicted by NMR

Figure 89

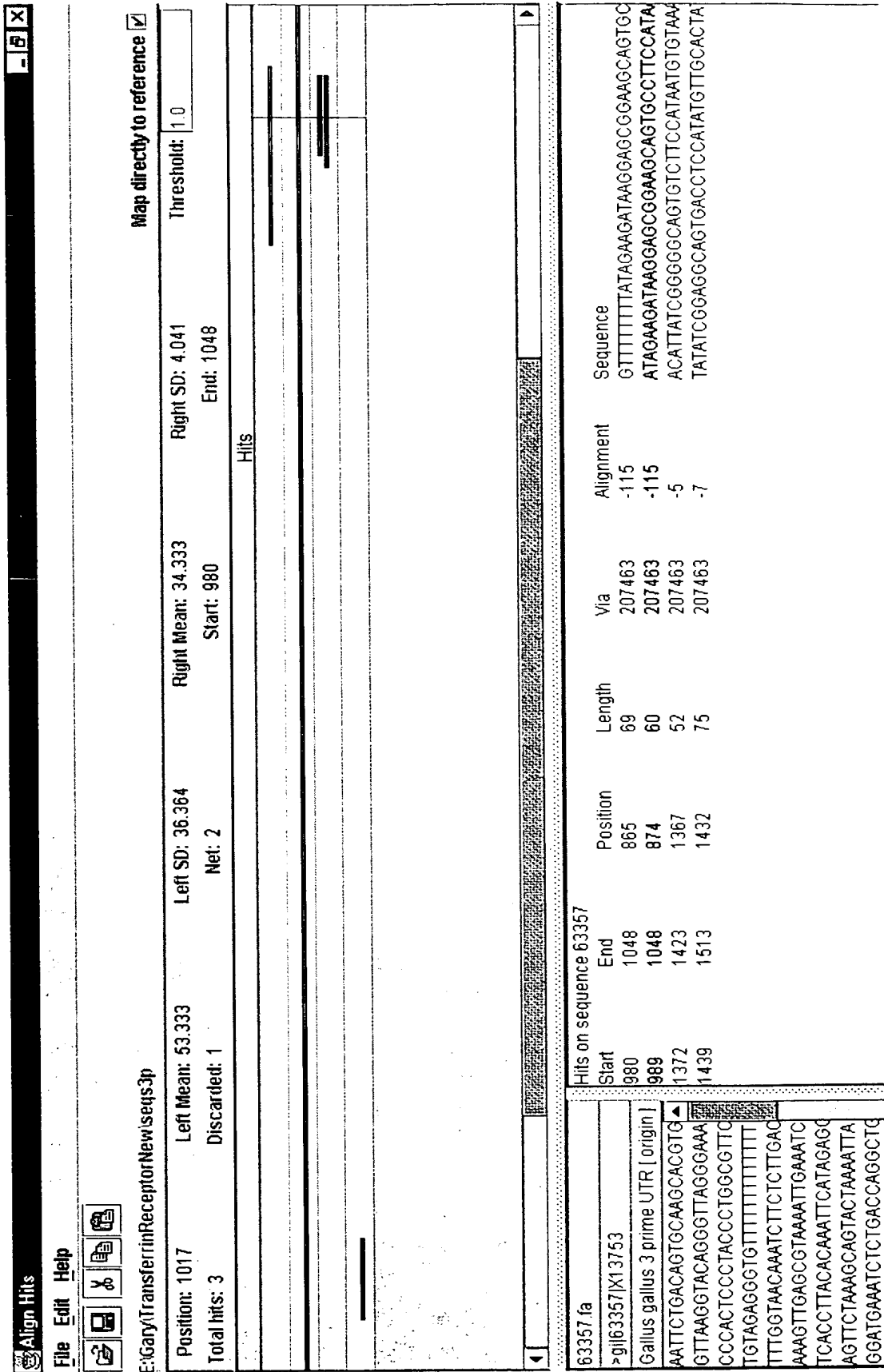


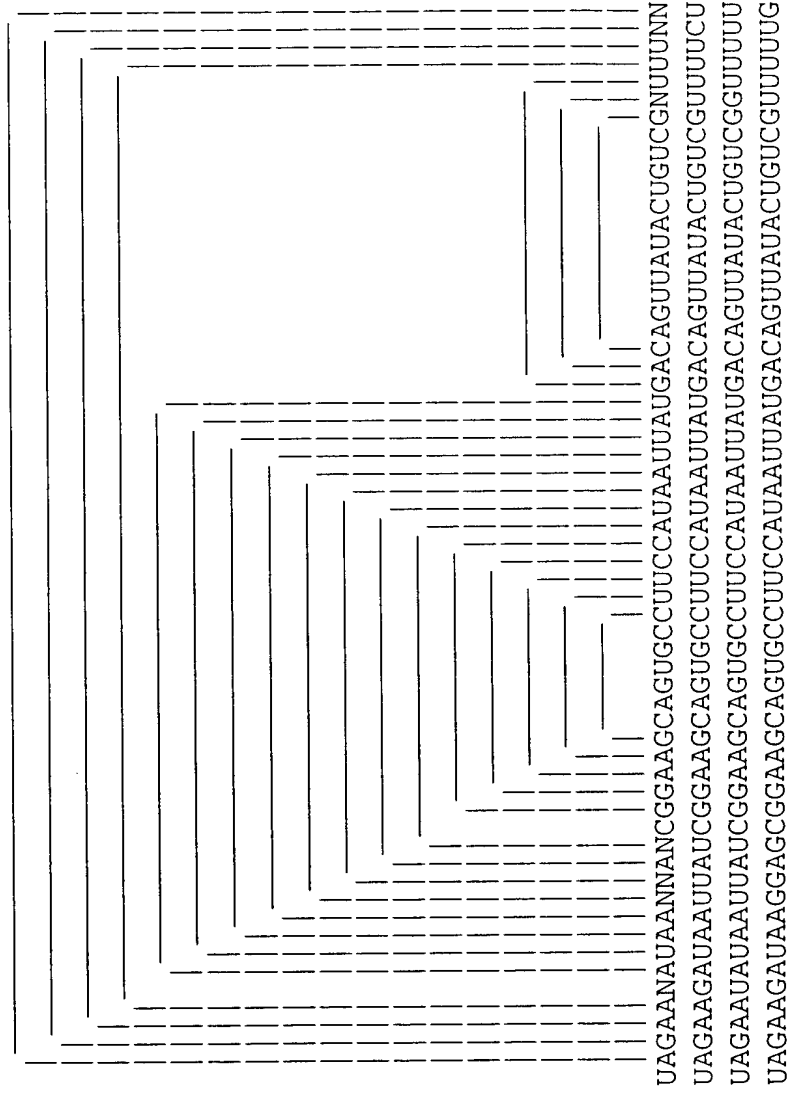
Figure 90

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
TAGAAGATAATTATCGGAAGCAGTGCCCTCCATAATTATGACAGTTATACTGTCGTTTTCT
gi|37432|X01060
TAGAATATAATTATCGGAAGCAGTGCCCTCCATAATTATGACAGTTATACTGTCGGTTTTT
gi|63357|X13753
TAGAAGATAAGGAGCGGAAGCAGTGCCCTCCATAATTATGACAGTTATACTGTCGTTTTTG
```

Figure 91

Score: 115.0



Consensus
gi|207463|M58040
gi|37432|X01060
gi|63357|X13753

Figure 92

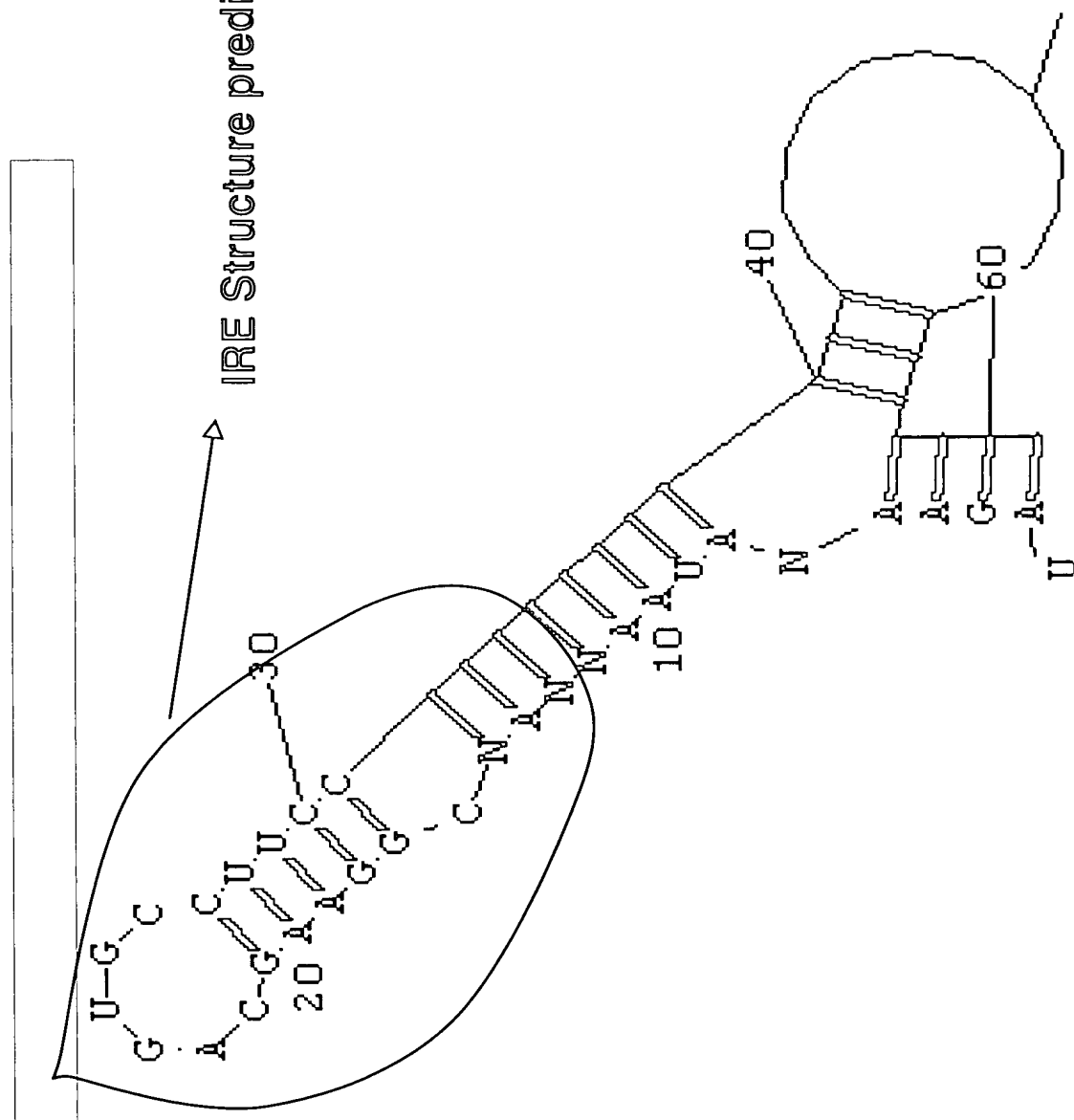


Figure 93

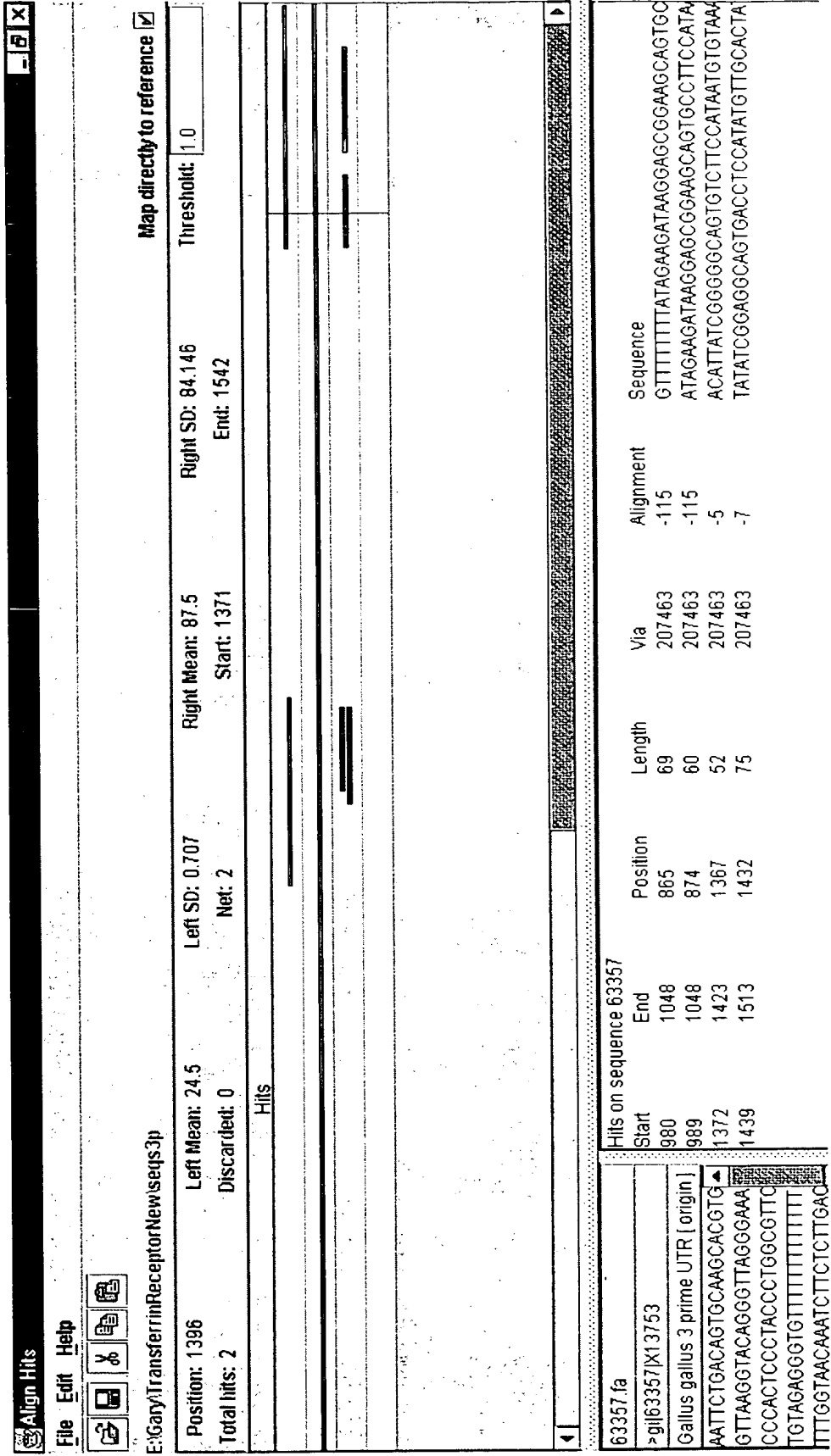


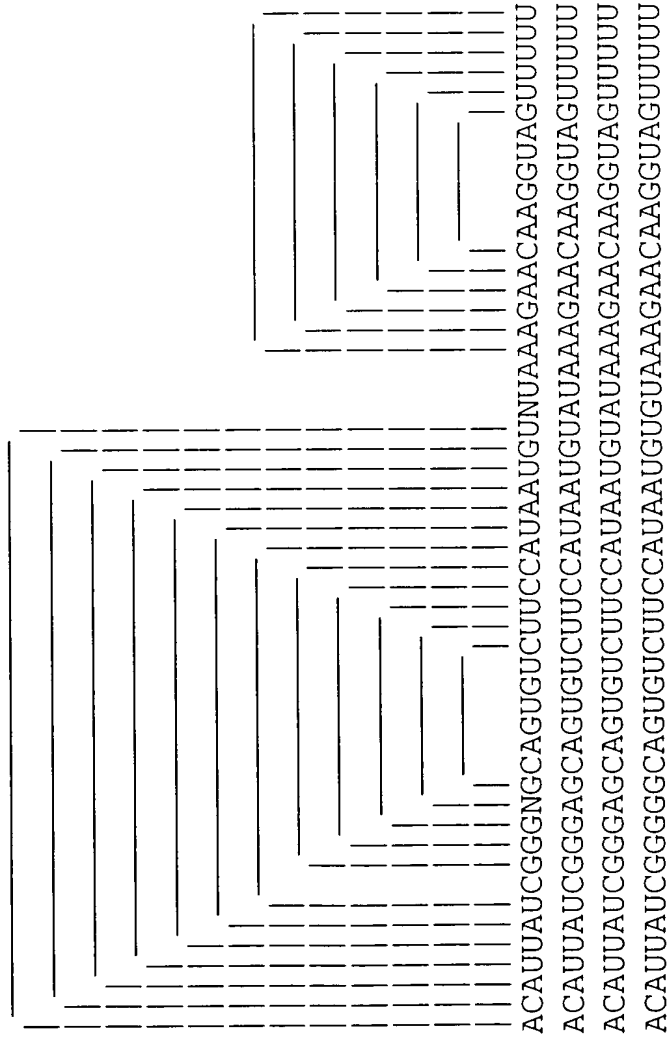
Figure 94

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGAACAAAGGTAGTTTTT
gi|37432|X01060      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGAACAAAGGTAGTTTTT
gi|63357|X13753      ACATTATCGGGGGCAGTGTCTTCCATAATGTGTAAAGAACAAAGGTAGTTTTT
*****
```

Figure 95

Score: 108.0



Consensus
gi | 207463 | M58040
gi | 37432 | X01060
gi | 63357 | X13753

Figure 96

Structure: 1 Energy = 108.0 nothing to say !

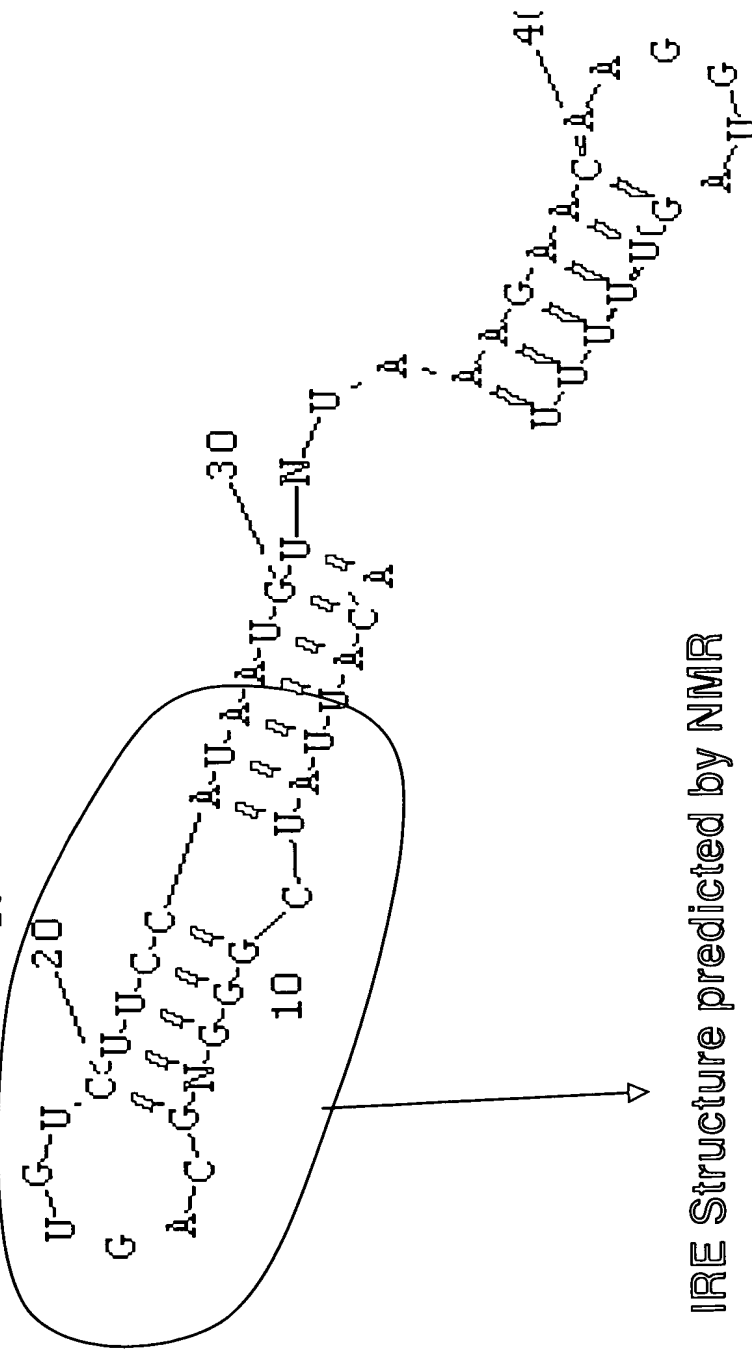


Figure 97

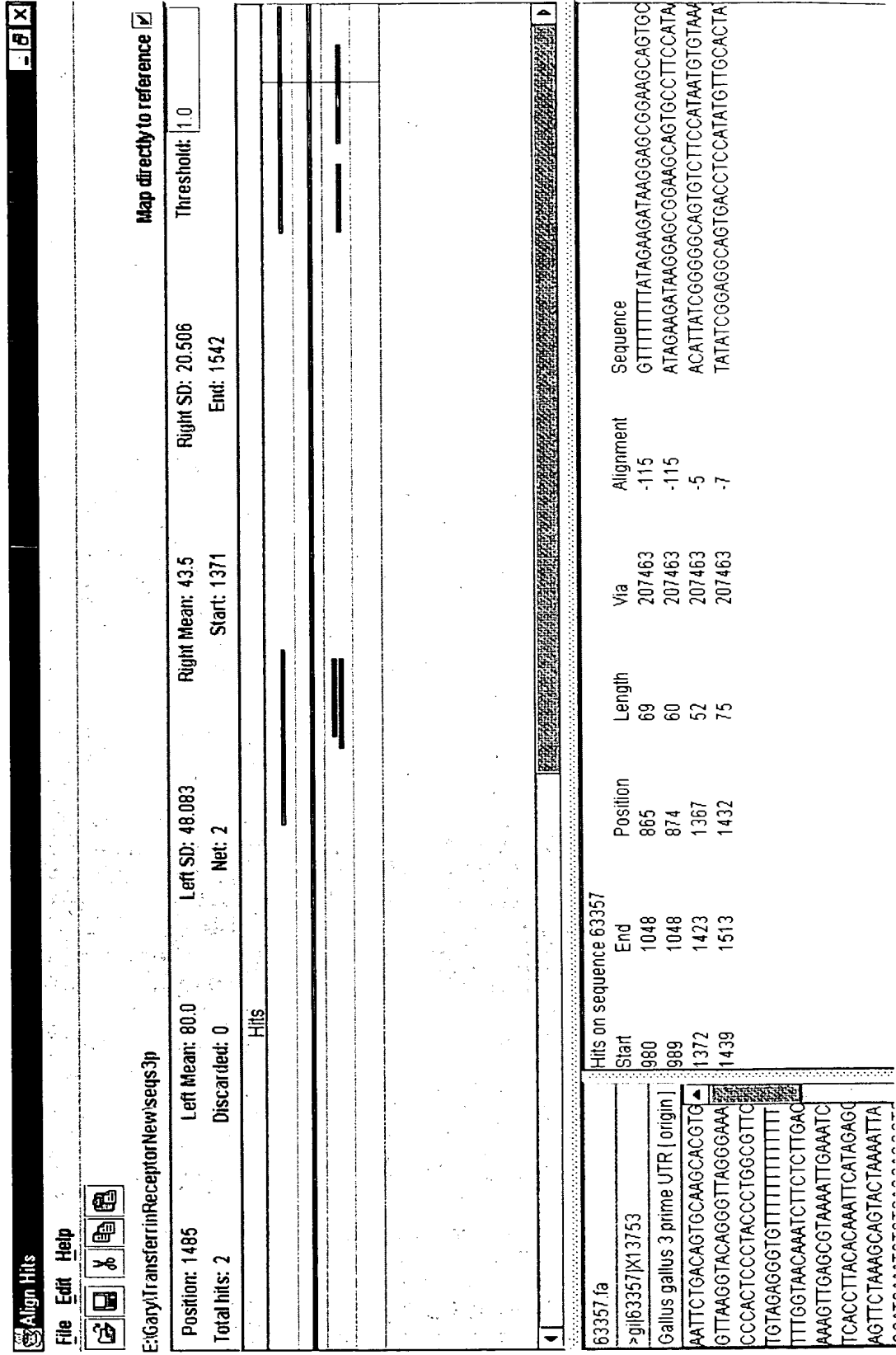


Figure 98

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      TATATCGGAGACAGTGACCTCCATATGTTACACTAAGGGTG
gi|37432|X01060      TGTATCGGAGACAGTGATCTCCATATGTTACACTAAGGGTG
gi|63357|X13753      TATATCGGAGGCAGTGACCTCCATATGTTGCACATATGGGGTG
* * * * *          * * * * *          * * * * *
```

Figure 99

Score: 78.0

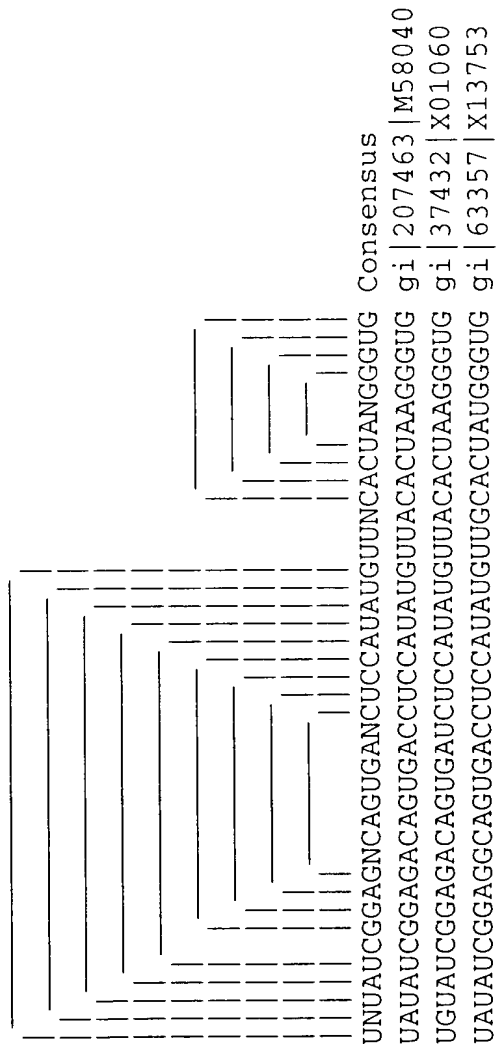
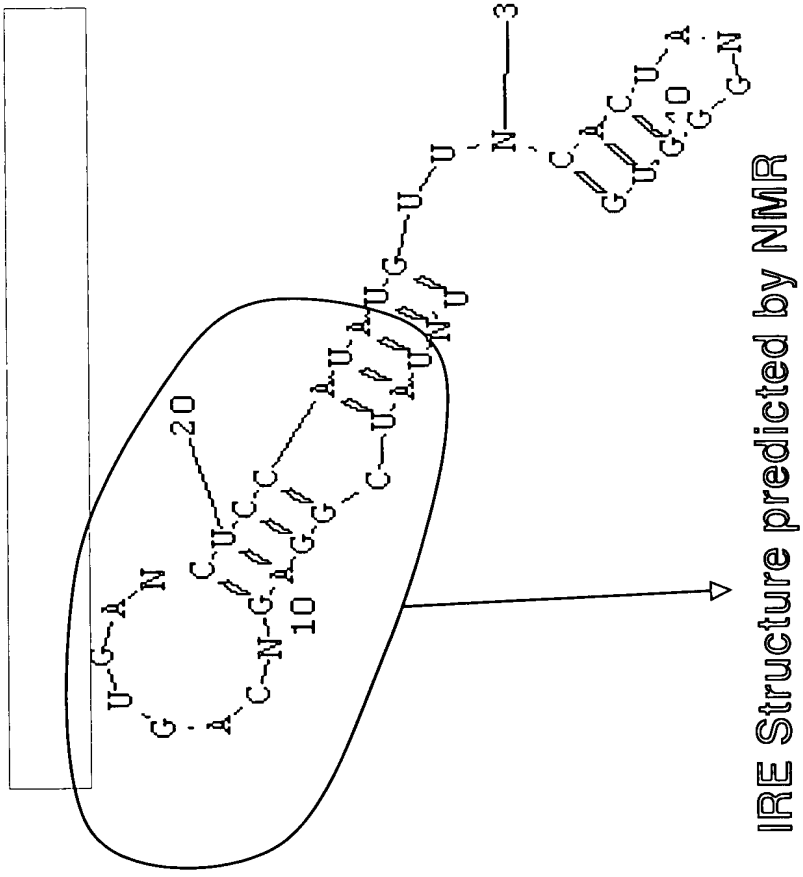


Figure 100



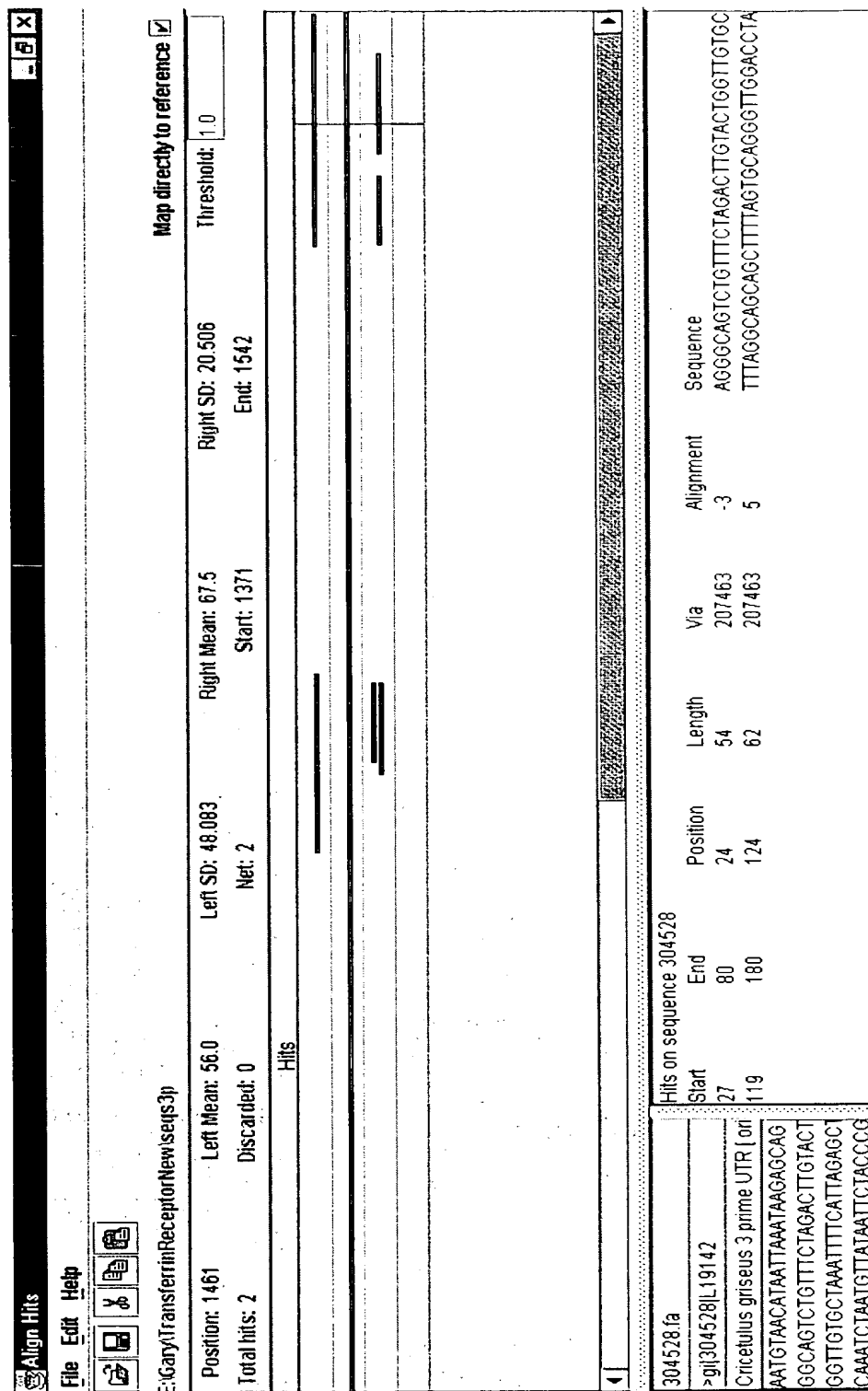


Figure 102

CLUSTAL W (1.74) multiple sequence alignment

gi 207463 M58040	GTACGTAATTATCGGGAACAGTGTTTCCCATAAATTTCTTCATGCGATGACATCTT
gi 37432 X01060	GTAAGTAATTATCGGGAACAGTGTTTCCCATAAATTTCTTCATGCAATGACATCTT
gi 63357 X13753	GTACGTAATTATCGGGGACAGTGTTTCCCATAAATTTCTTCATGAAATGTCATCTG

Figure 103

Score: 84.0

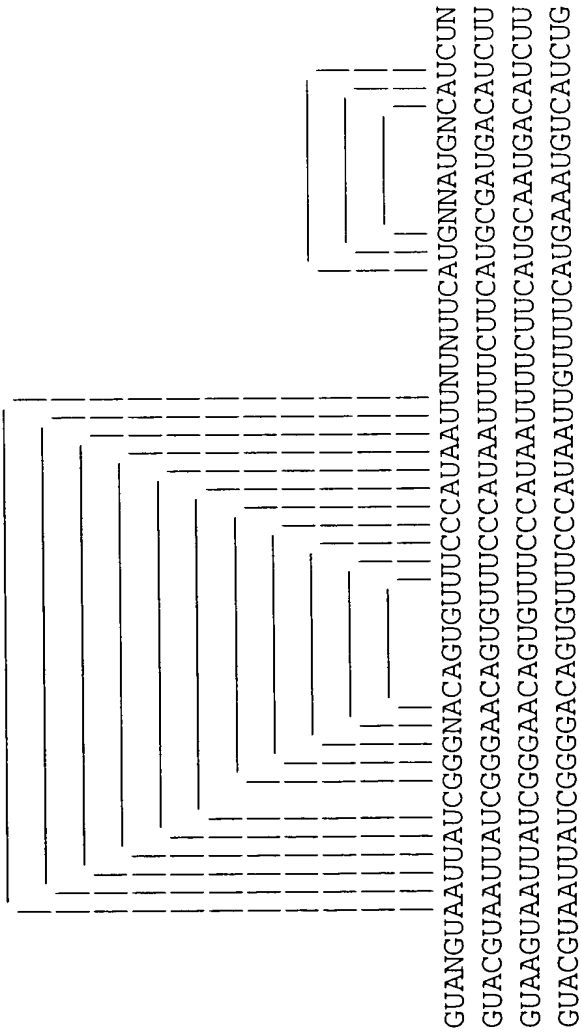


Figure 104

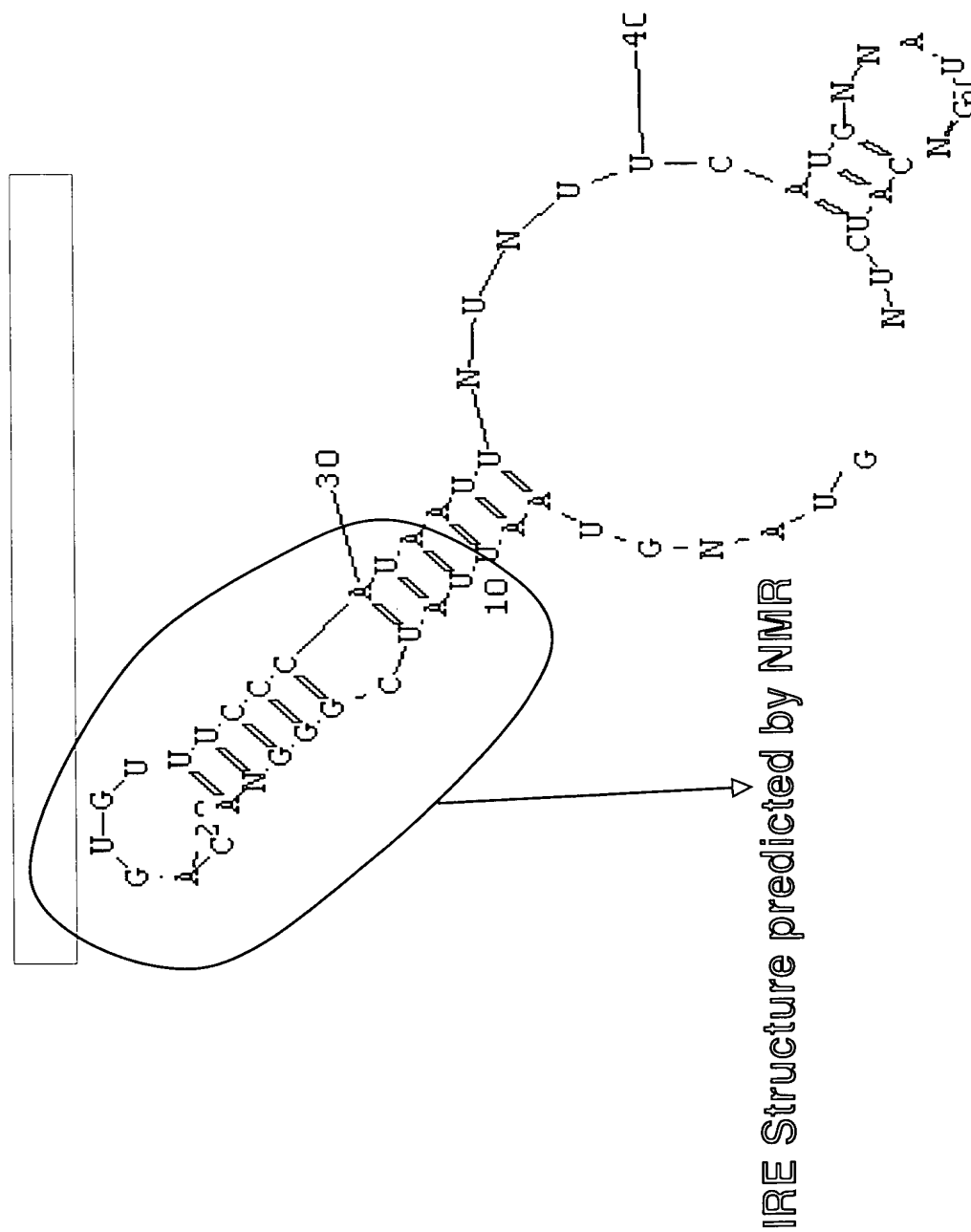
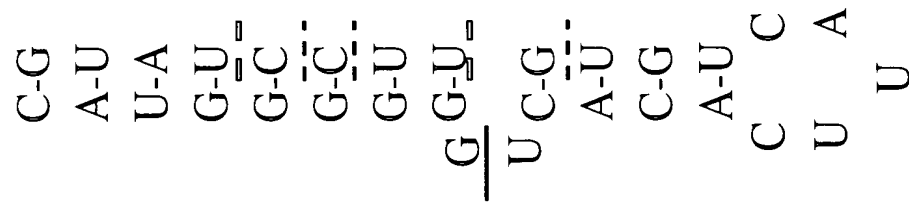
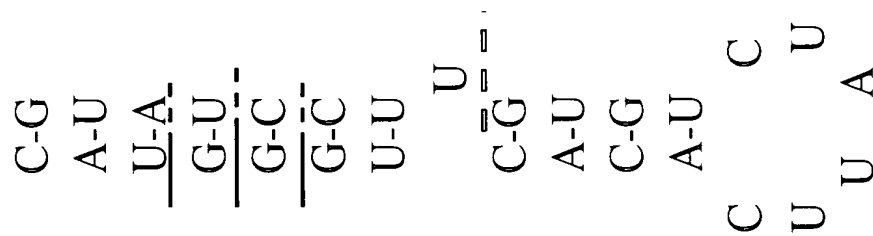


Figure 105



404561



35135

Y ion

C ion



Figure 106

CLUSTAL W (1.74) multiple sequence alignment		A	
1			
2			
3			
4	gi 163448 M92441	-ACTGGGAGATGGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAAATAT----	
5	gi 163448 M92441b	---TGGGAGATGGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAAATATTT--	
6	gi 200123 M87223	--CTAGAAGATGGGGG-TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTG-	
7	gi 200123 M87223b	---TAGAAGATGGGGG-TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTGT	
8	gi 205807 J04791	--CTAGGAGATGGGGG-TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTT-	
9	gi 205807 J04791b	---TAGGAGATGGGGG-TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTTA	
10	gi 35135 X55362	--CTAGGATATGGG---TCACACTTATCTGTGTTCCCTATGGAACCTATTGAAATATTT--	
11	gi 404561 S64539	----AGGAGATGGGGGTCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTGT	
12	gi 404561 S64539b	---TAGGAGATGGGGGTCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAAATATTTG-	
13	gi 63712 X64710	--CTAGGAGATGGG---TCACATTTATCTGTGTTCCCTATGGAACCTATTGAAATATTG--	
14	gi 63712 X64710b	GACTAGGAGATGGG---TCACATTTATCTGTGTTCCCTATGGAACCTATTGAAATAT----	
15	gi 64953 X56316	-ACTGCGAGATGGGG--TCACA--TATCTGTGTTCCCTATGGAACCTTTTTTTTTTTC--	
16		* * * * *	** * * * * * * * * * * * * * *
17		NNNNNNNANATGGGNNNTACANNTANCTGTGTTCCCTATGGAACCTNNNTTNNNTNNNN	
18			

Figure 107

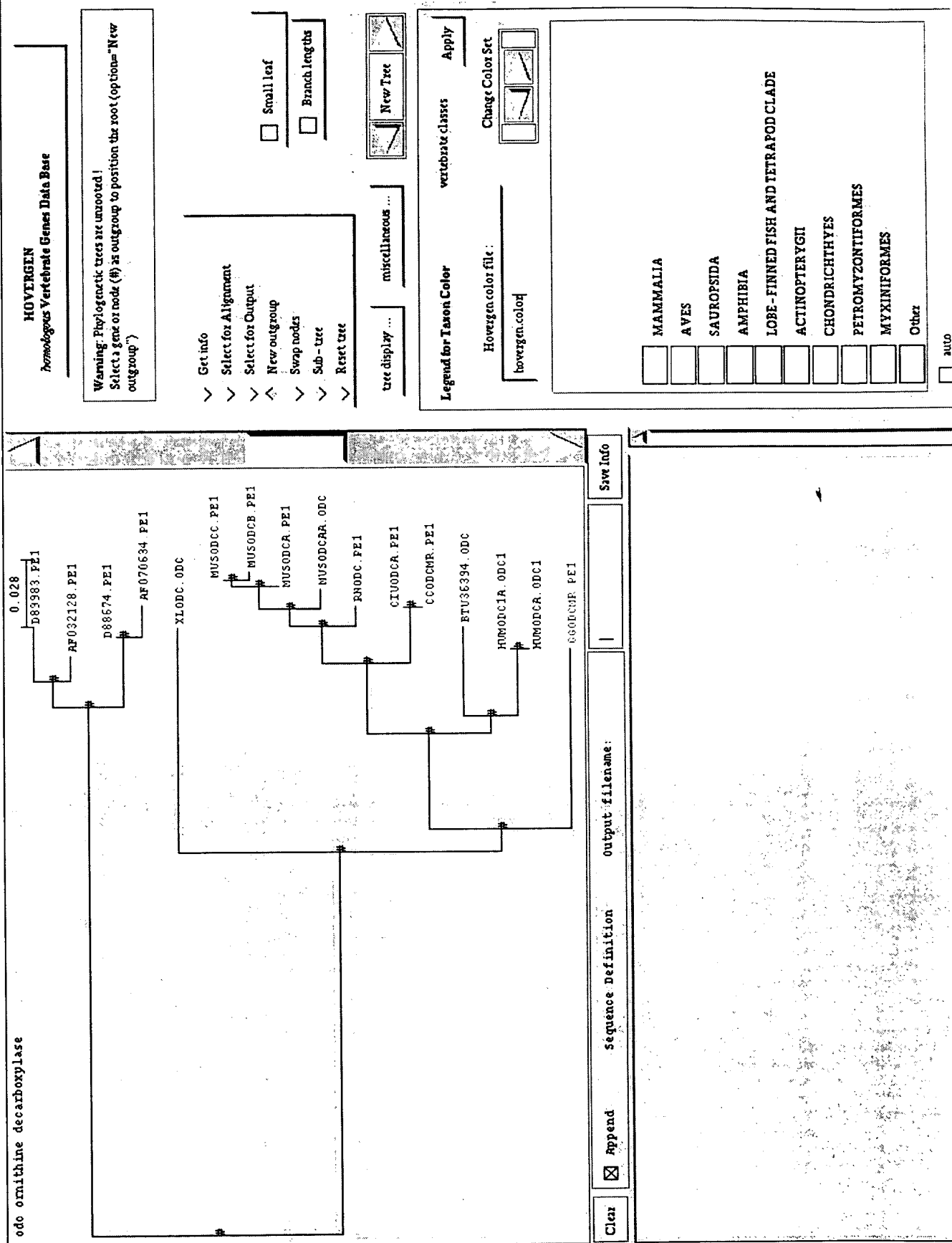


Figure 108

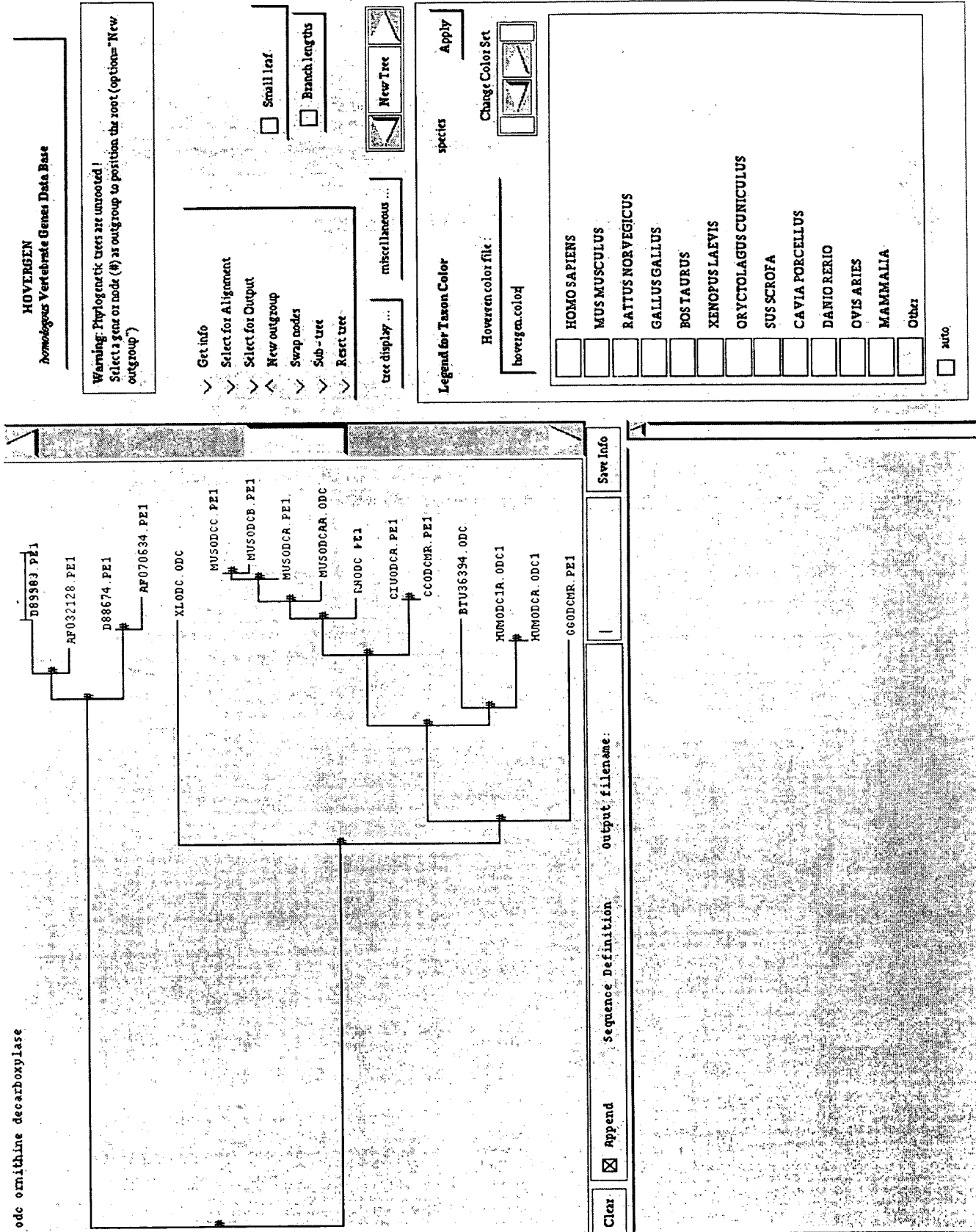


Figure 109

J:\cowxTargets\35135\seqs3p

Position:		Left Mean:	Left SD:	Right Mean:
Total hits:		Discarded:	Net:	Start:
Number	Description		Hits	
<input type="checkbox"/> 35135.fa	Homo sapiens 3 prime UTR ...			
<input checked="" type="checkbox"/> 64953.fa	Xenopus laevis 3 prime UTR...			
<input type="checkbox"/> 162173.fa	Trypanosoma brucei 3 prime...			
<input type="checkbox"/> 163448.fa	Bos taurus 3 prime UTR [ori...			
<input type="checkbox"/> 205807.fa	Rattus norvegicus 3 prime U...			
<input type="checkbox"/> 404561.fa	Mus musculus domesticus ...			
<input type="checkbox"/> 63712.fa	Gallus gallus 3 prime UTR [...			
<input type="checkbox"/> 200123.fa	Mus pahari 3 prime UTR [ori...			
<input type="checkbox"/> 2337849.fa	Ustilago maydis 3 prime UT...			

Region 1

Region 2

Figure 110

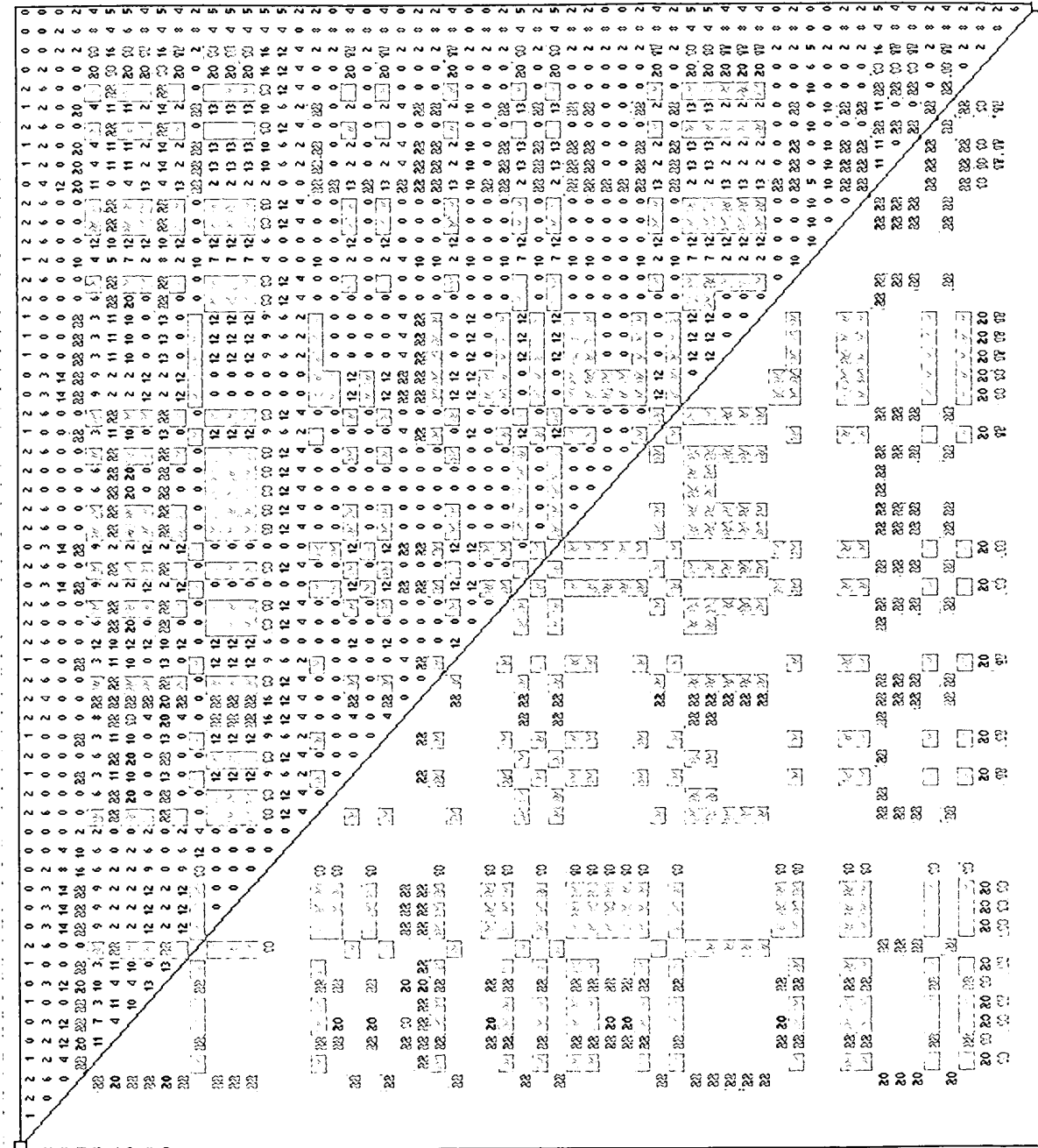


Figure 111

Score: 300.0

```
NNNNNNNANAUUGGNNNNNACACANNNUANCUGUGUCCUAUGGAAACUUNNUUNNNUNNNNN
-ACUGGGAGAUUGGG--UCACACUUAUCUGUGUCCUAUGGAAACUAUUUGAAUAU----
---UGGGAGAUUGGG--UCACACUUAUCUGUGUCCUAUGGAAACUAUUUGAAUAUU--
--CUAGAAGAUUGGGG-UCACACUUA-CUGUGUCCUAUGGAAACU--UUGAAUAUUUG-
--UAGAAGAUUGGGG-UCACACUUA-CUGUGUCCUAUGGAAACU--UUGAAUAUUUGU
--CUAGGAGAUUGGGG-UCACACUUA-CUGUGUCCUAUGGAAACU--UUGAAUAUUUU-
---UAGGAGAUUGGGG-UCACACUUA-CUGUGUCCUAUGGAAACU--UUGAAUAUUUUA
--CUAGGAUAUGGG--UCACACUUAUCUGUGUCCUAUGGAAACU--UUGAAUAUUUU-
---AGGAGAUUGGGGGUCACACUUA-CUGUGUCCUAUGGAAACU--UUGAAUAUUUGU
---UAGGAGAUUGGGGGUCACACUUA-CUGUGUCCUAUGGAAACU--UUGAAUAUUUG-
--CUAGGAGAUUGGG--UCACAUUUUUCUGUGUCCUAUGGAAACU--UUGAAUAUUUG--
GACUAGGAGAUUGGG---UCACAUUUUUCUGUGUCCUAUGGAAACU--UUGAAUAU---
-ACUGCGAGAUUGGG--UCACA--UAUCUGUGUCCUAUGGAAACUUUUUUUUUUUUC--
```

Consensus

gi|163448|M92441
gi|163448|M92441b
gi|200123|M87223
gi|200123|M87223b
gi|205807|J04791
gi|205807|J04791b
gi|35135|X55362
gi|404561|S64539
gi|404561|S64539b
gi|63712|X64710
gi|63712|X64710b
gi|64953|X56316

Figure 112

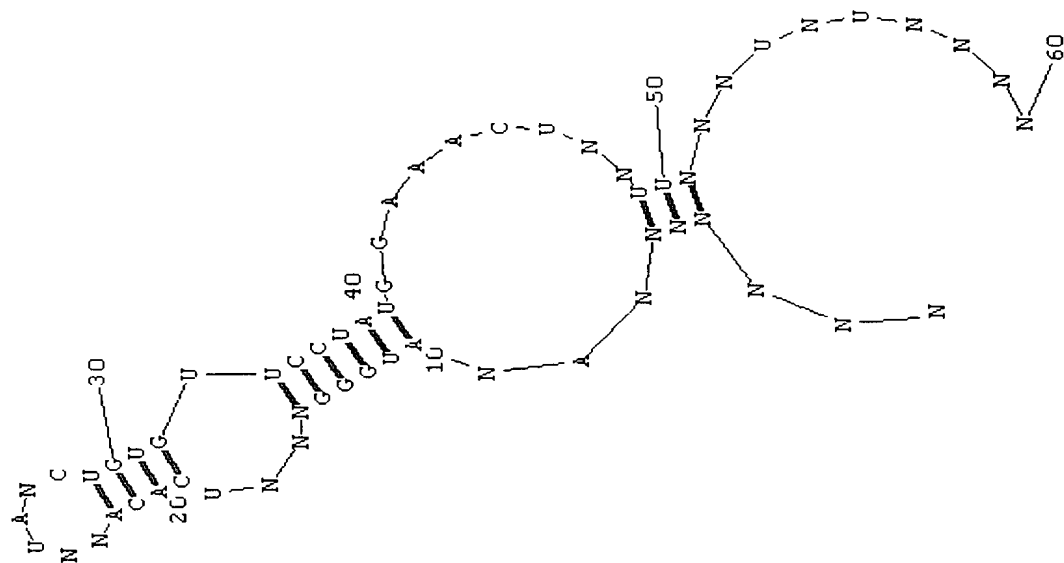
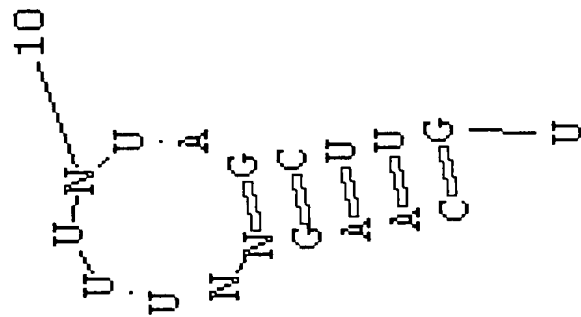


Figure 113

CLUSTAL W (1.74) multiple sequence alignment

```
gi|404561|S64539      CAAAGCGTTTGTAGCTTGT
gi|63712|X64710      CAAATATTGTAGCTTGT
gi|64953|X56316      CAAAGCATTTGTAGCTTGT
gi|35135|X55362      CAAAGCATTTGTAGCTTGT
gi|200123|W87223      CAAAGCATTTATAGCTTGT
gi|205807|J04791      CAAAGCATTTGTAGCTTGT
***** **
```


Figure 115



Case	Age	Sex	Duration of illness	Site of lesion	Pathological findings	Microscopic findings	Immunohistochemical findings	Diagnosis
1	65	M	10 years	Left frontal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
2	55	F	5 years	Right parietal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
3	45	M	3 years	Left temporal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
4	35	F	2 years	Right frontal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
5	25	M	1 year	Left parietal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
6	15	F	6 months	Right frontal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
7	10	M	3 months	Left frontal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
8	5	F	2 months	Right parietal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
9	3	M	1 month	Left temporal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma
10	1	F	2 weeks	Right frontal lobe	Large, well-circumscribed, solid, grayish-white mass	Neurons and glial cells	Neurons: +, glial cells: +	Low-grade glioma



Figure 117

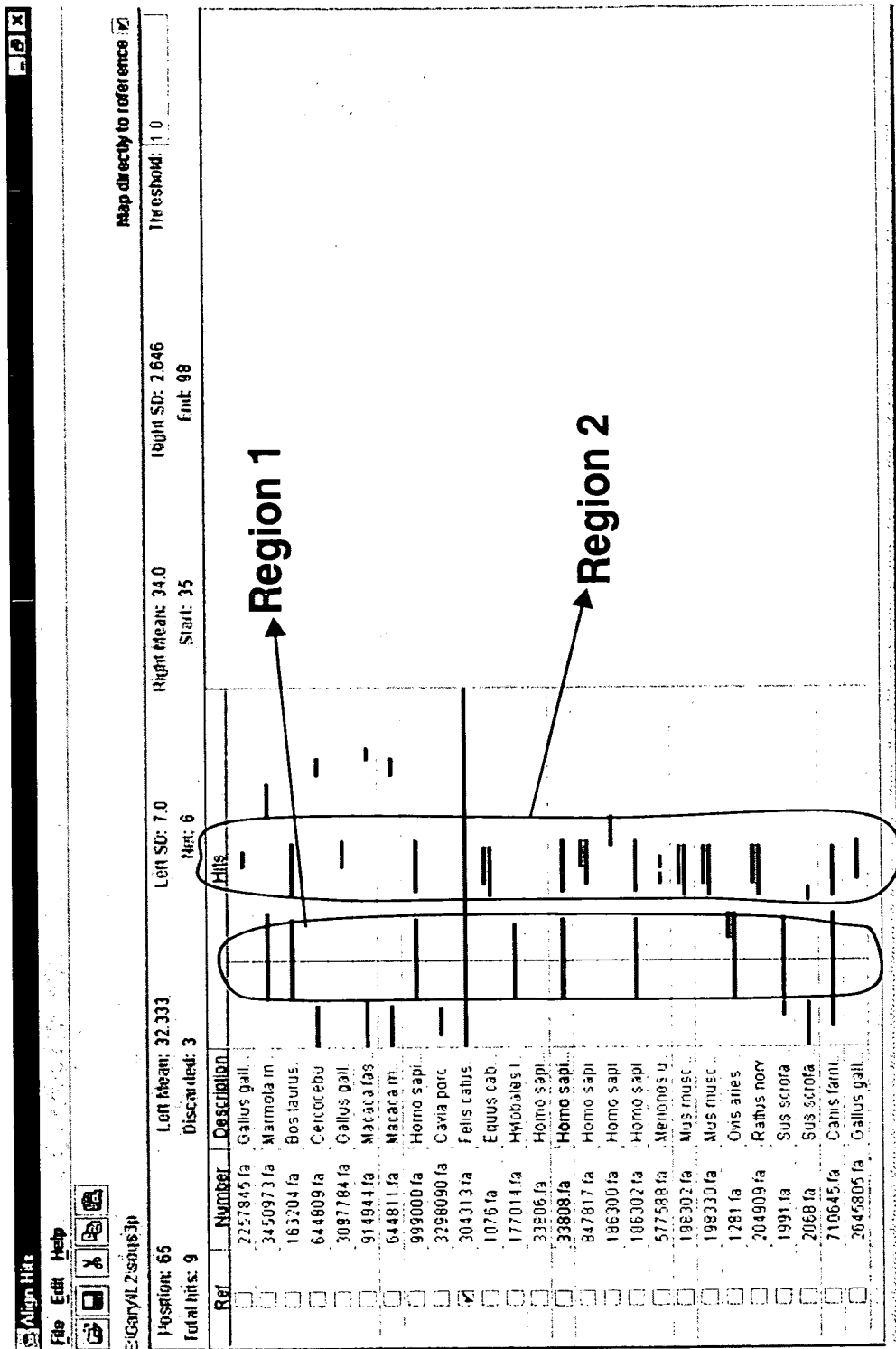


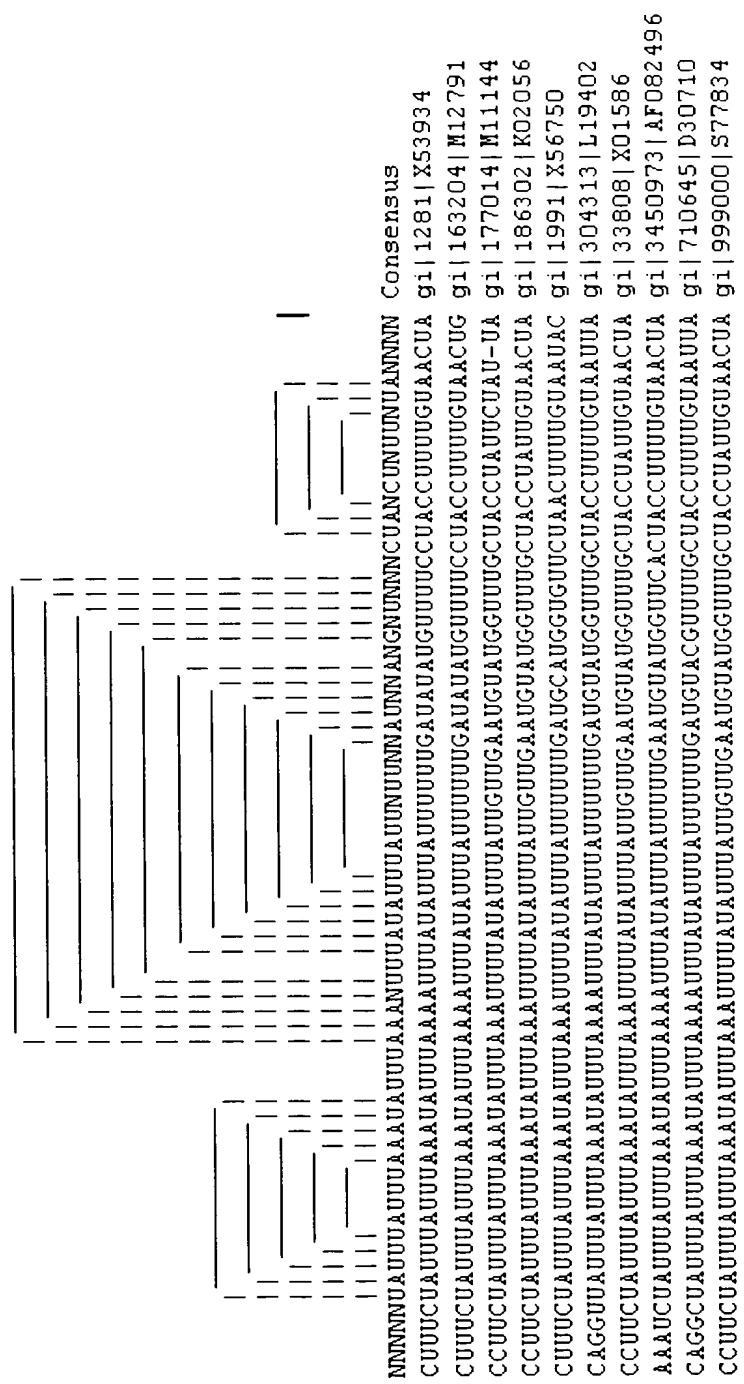
Figure 118

CLUSTAL W (1.74) multiple sequence alignment

```
gi|1281|X53934      CTTTCTATTTTAAATATTTAAATTTTATATTTATTTTGTGATATATGTTTTCTCTACCTTTTGTAACTA
gi|163204|M12791    CTTTCTATTTTAAATATTTAAATTTTATATTTTGTGATATATGTTTTCTCTACCTTTTGTAACTG
gi|177014|M11144    CCTTCTATTTTAAATATTTAAATTTTATATTTATGTTGAATGATGGTTTGTCTACCTATTTCTAT-TA
gi|186302|K02056    CCTTCTATTTTAAATATTTAAATTTTATATTTATTTGTTGAATGATGTTTGTCTACCTATTTGTAACTA
gi|1991|X56750      CTTTCTATTTTAAATATTTAAATTTTATATTTATTTTGTATGTCATGGTGTCTAACTTTTGTAAATAC
gi|304313|L19402    CAGGTTATTTTAAATATTTAAATTTTATATTTATTTTGTATGATGGTTTGTCTACCTTTTGTAAATTA
gi|33808|X01586     CCTTCTATTTTAAATATTTAAATTTTATATTTATTTGTTGAATGATGGTTTGTCTACCTATTTGTAACTA
gi|3450973|AF082496 AATCTATTTTAAATATTTAAATTTTATATTTATTTTGAATGATGTTTGTCTACCTTTTGTAACTA
gi|710645|D30710    CAGGCTATTTTAAATATTTAAATTTTATATTTATTTTGTATGTCATGGTTTGTCTACCTTTTGTAAATTA
gi|999000|S77834    CCTTCTATTTTAAATATTTAAATTTTATATTTATTTGTTGAATGATGTTTGTCTACCTATTTGTAACTA
```

Figure 119

Score: 404.0



100% pure and free from any other impurities. The product is a white, crystalline solid.

Figure 120

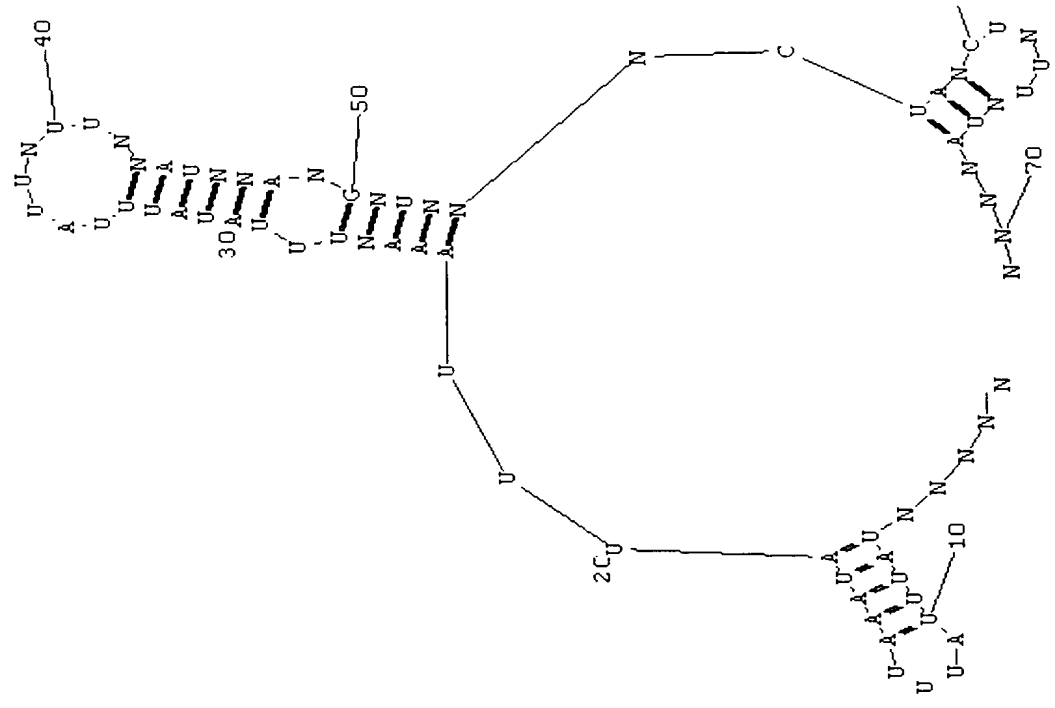


Figure 121

CLUSTAL W (1.74) multiple sequence alignment

91	1076	X69393	TGATAAATATG--GATCTTTTAAGATTCTTTTGTAG-CCCCXXXXXX-
91	163204	M12791	TGATAAATATG--GATCTTTTAAGATTCTTTTGTAG-CCCTACGGGC-
91	186300	W22005	XXXXXXXXXX--XXXXXXXXXXXXXXXXXXXXXXTCCACCC TGA--
91	186302	K02056	CTATAAATATG--GATCTTTTATGATTC TTTGTAG-CCCTACGGGC-
91	198302	K02797	TGATAAATATG--GATCTTTAAAGATTCTTTTGTAGCCCCCAAGGC--
91	198330	K02292	TGATAAATATG--GATCTTTAAAGATTCTTTTGTAGCCCCCAAGGC--
91	204909	W22899	TGATAAATATG--GATCTTTAAAGATTCTTTTGTAGCCCCCAAGGC--
91	2068	X58428	TCTTAAATGTATCAGCGCXXXXXXXXXXXXXXXXXXXXXX-XXXXXX----
91	2257845	AF000631	-CTCTCTTCTAA-GATCATATTTGATCCTTTCTGTAA--CCTACGGGCTC
91	2645805	AF033563	-CTCTCTTCTAA-GATCATATTTGATCCTTTCTGTAGCCCTACGGGC--
91	304313	L19402	TGATAAACATG--GATCTTTTAAAGATTCTTTTGTAG-CCCTACGGGT-
91	3087784	AJ224516	-CTCTCTTCTAA-GATCATATTTGATCCTTTCTGTAGCCCTACGGGC--
91	33808	X01586	CTATAAATATG--GATCTTTTATGATTC TTTTGTAG-CCCTACGGGC-
91	577588	X68779	CGATAAATATG--GATCTTTAGAGATTCTTTTGTAG--CCCAAGGGCTC
91	710645	D30710	TGATAAATATG--GATCTTTTAAAGATTCTTTTGTAG-CCCCXXXXXX-
91	847817	U25676	CTATAAATATG--GATCTTTTATGATTC TTTTGTAG-CCCTACGGGC-
91	999000	S77834	CTATAAATATG--GATCTTTTATGATTC TTTTGTAG-CCCTACGGGC-

Figure 122

Score: 412.0

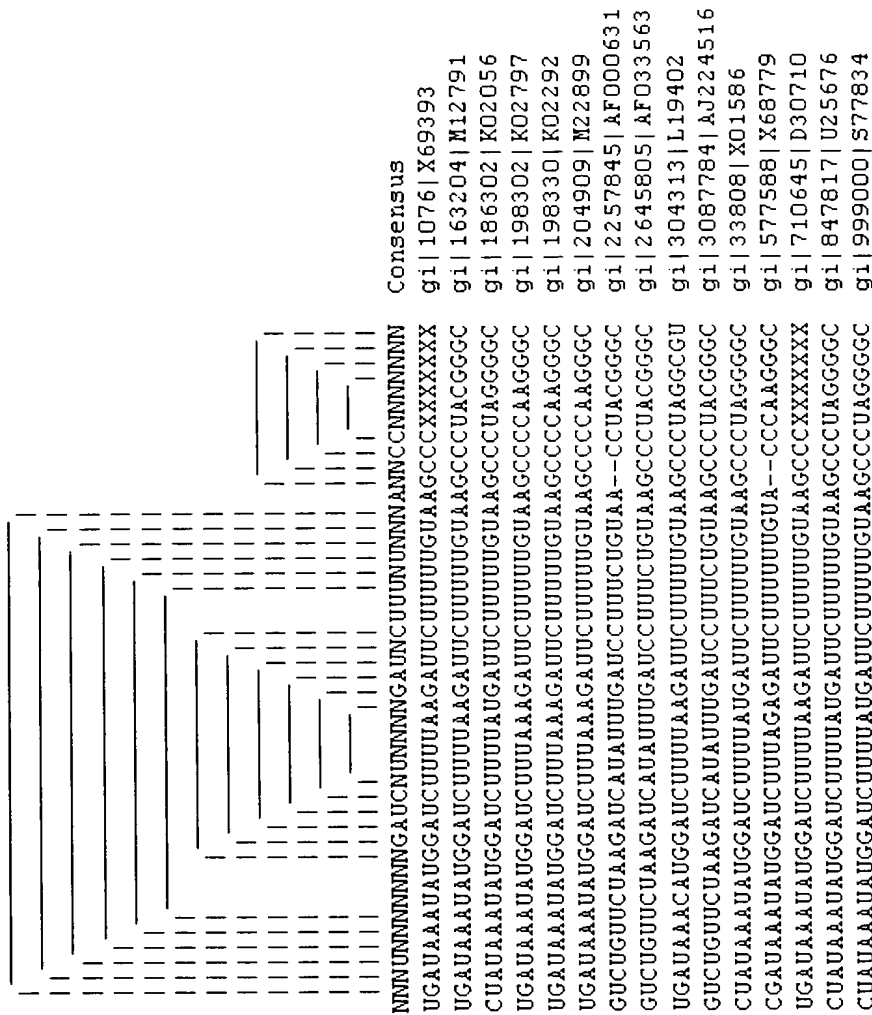


Figure 123

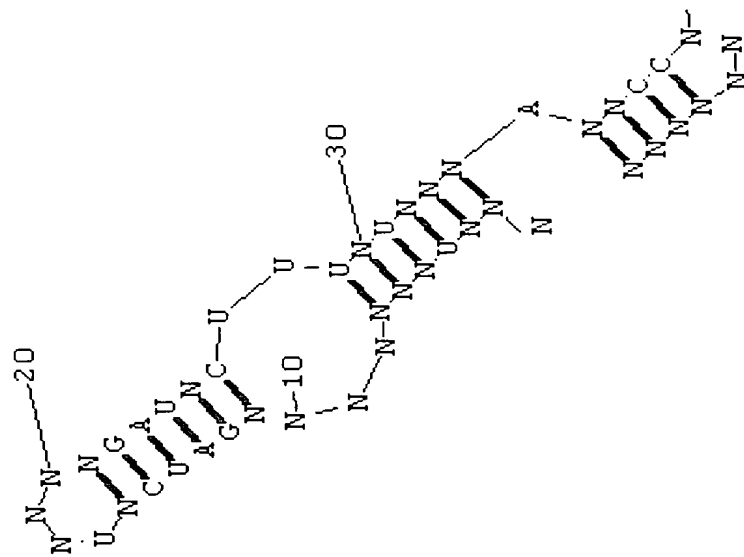


Figure 124

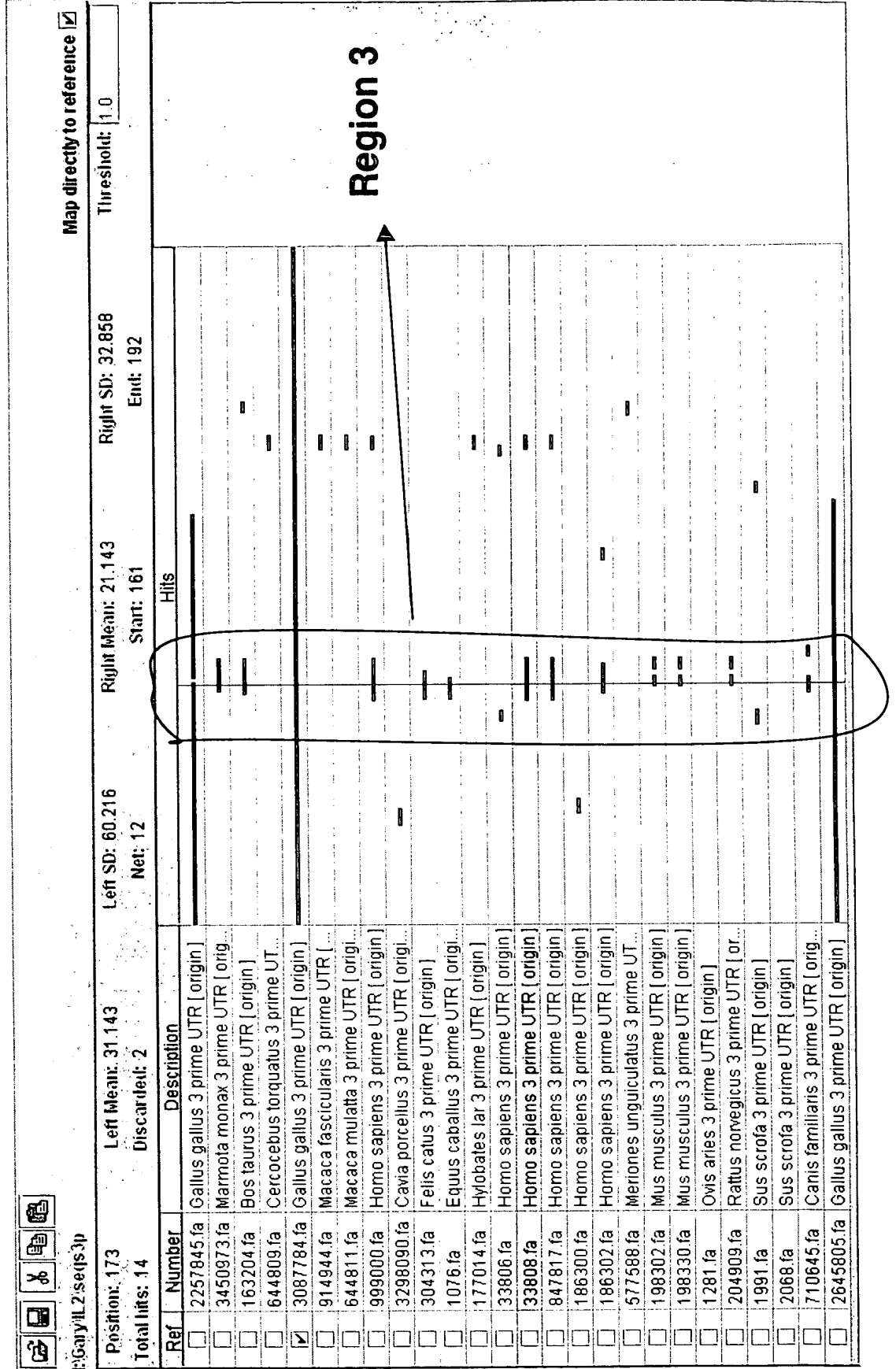


Figure 125

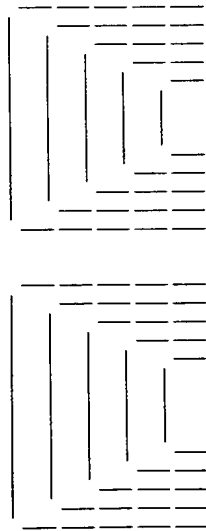
CLUSTAL W (1.74) multiple sequence alignment

gi 163204 M12791	-TTTTAAGATTCTTTTGTAGCCCTACGGGCT-TAAAAATTCA
gi 304313 L19402	-TTTTAAGATTCTTTTGTAGCCCTAGGCGTGCTAAAAACTC-
gi 198302 K02797	-TTTTAAGATTCTTTTGTAGCCCCCAAGGGCTCAAAAATGTT-
gi 204909 M22899	-TTTTAAGATTCTTTTGTAGCCCCCAAGGGCTCAAAAATGTT-
gi 3450973 AF082496	CTTTAAGATTCTTTT-GTAAGCCCTAAGGGCTCTAAAAATGGT-
gi 33808 X01586	-TTTTATGATTCTTTTGTAGCCCTAGGGGCTCTAAAAATGGT-
gi 3087784 AJ224516	-ATATTTGATCCTTTTCTGTAGCCCTACGGGCTCAAAAATGTAC-

* * * * * * * * * * * * *

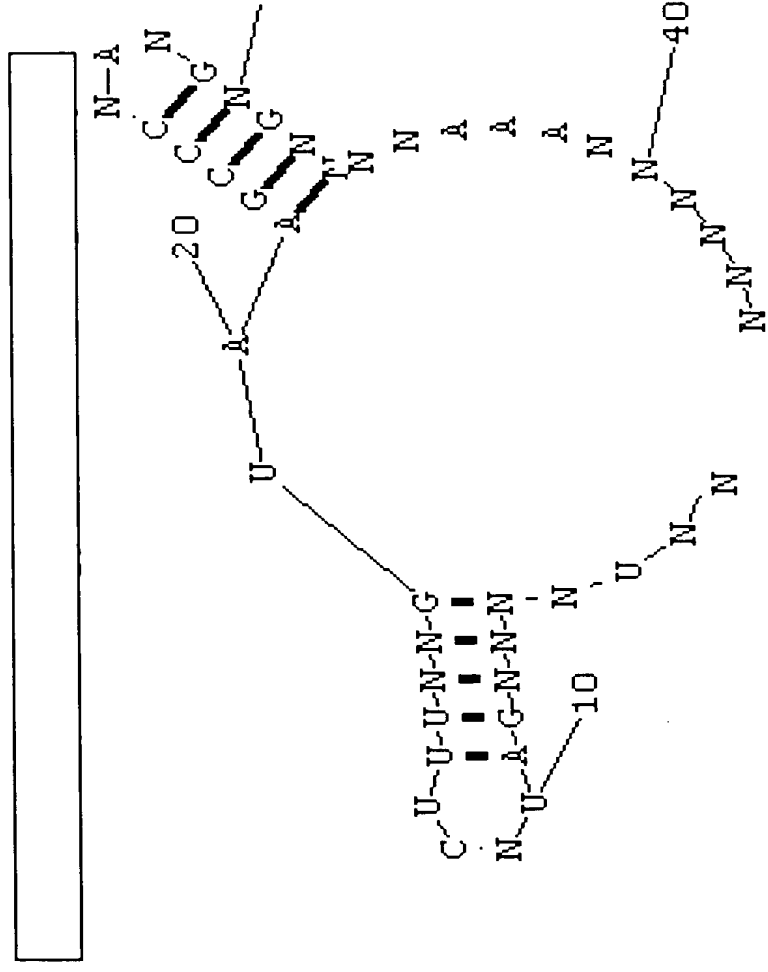
Figure 126

Score: 165.0



Consensus	
gi	163204 M12791
gi	304313 L19402
gi	198302 K02797
gi	204909 M22899
gi	3450973 AF082496
gi	33808 X01586
gi	3087784 AJ224516

Figure 127



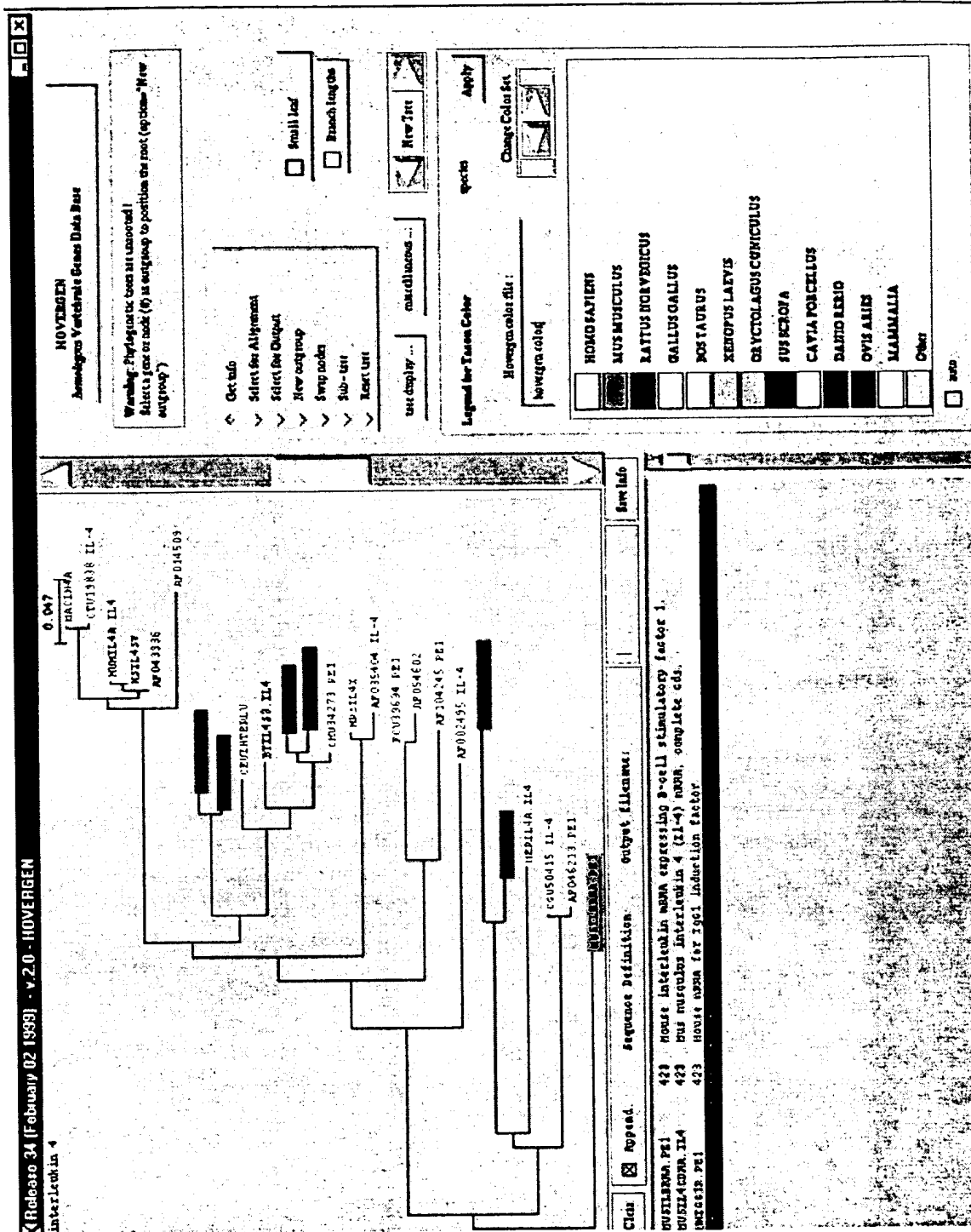
[illegible]

Figure 129

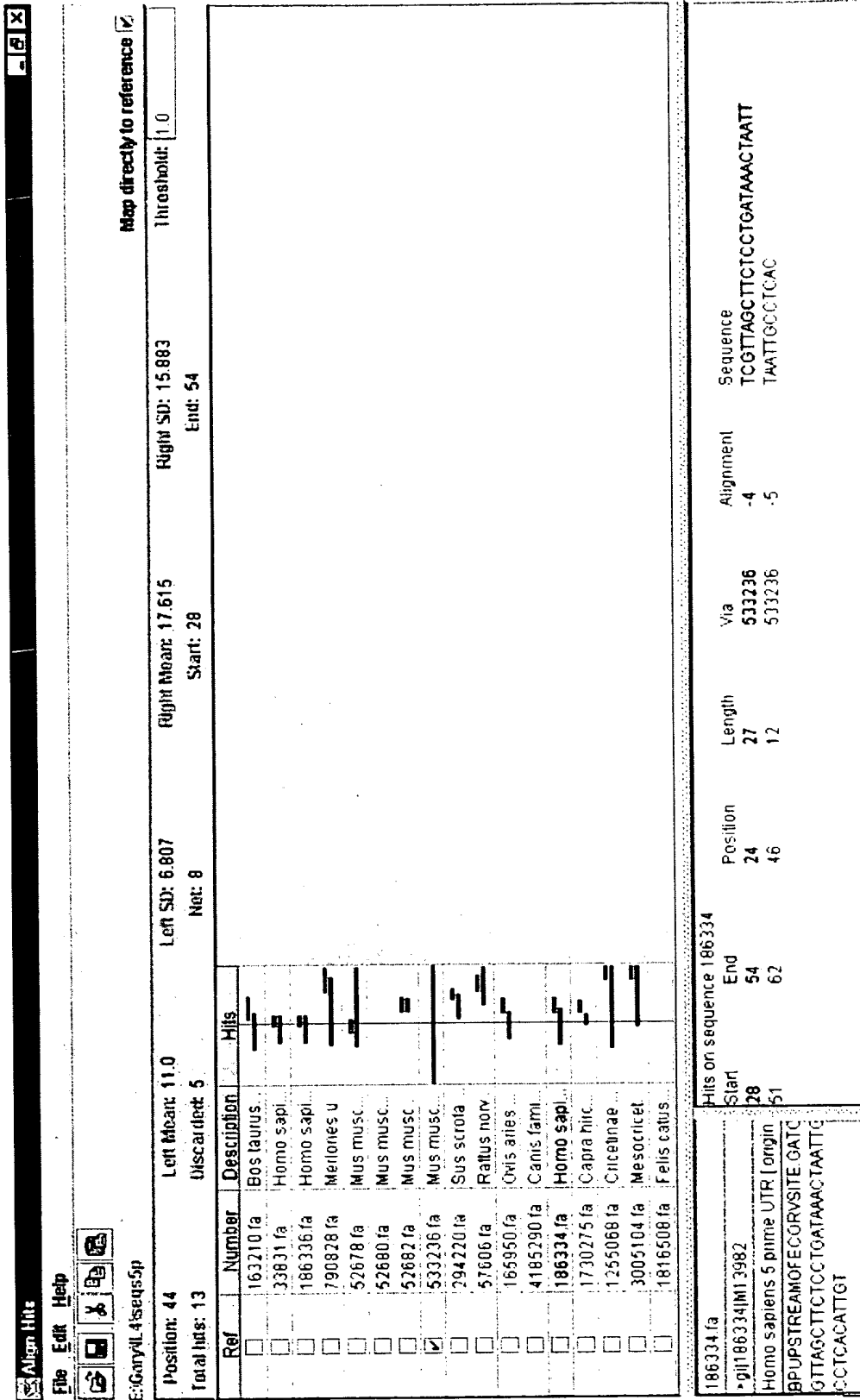


Figure 130

CLUSTAL W (1.74) multiple sequence alignment

gi 1255068 U50415	XXXTGCA	TTGTTAGCGTCTCTTGATAACCTTAAT-TGTCCTCTATCACTGA---
gi 163210 M77120	-XXXXTGCA	TTGTTAGCGTCTCTCTGGTAAACTAAATTGTCTCACATTGTCACT--
gi 165950 M96845	-XXXXXXXXXX	TAGCTTCTCCTGATAATCTAATTGCCCTCACACTGTCAGT--
gi 1730275 U34273	-XXXXXXXXXX	TAGCTTCTCCTGATAAACTAAATTGTCTCACACTGTCAGT--
gi 186334 M13982	-----GATCGTT	AGCTTCTCCTGATAAACTAAATTGCCCTCACATTGTGTXXX---
gi 186336 M23442	-GCATTGCAT	CGTTAGCTTCTCCTGATAAACTAAATTGCCCTCACATTGTCACT--
gi 294220 L12991	---XXXXXX	XXXXXXXXXXXXXXGGTAAACTAAATTGTCTCACATCGTCAGTGC
gi 3005104 AF046213	XXXXXXXXXX	XXXXXXXXXXXXXXTTGATAACCTTAATTGTCTCTATCACTGA---
gi 33831 X06750	-GCATTGCAT	CGTTAGCTTCTCCTGATAAACTAAATTGCCCTCACATTGTCACT--
gi 52678 X05064	GCATTGCAT	TTGTTAGCATCTCTTGATAAACTTAATTGTCTCTCGTCACTGA---
gi 52678 X05064b	-GTGTGCGCA	AGGCAGACTTCTTGATA-TTACTCTGTCTTTCCCCAGGGCGA-
gi 52682 X05253	XXXXXXXXXX	CCCCAGGCCGACAGCGAGACCCAAATCTGTCTCACAAATGAAC---
gi 533236 M25892	GGGGGGATT	TGTTAGCATCTCTTGATAAACTTAATTGTCTCTCGTCACTGA---
gi 790828 L37779	XXXXXXXXXA	TTGTTGGCATCTCTTGACAAACTTAATTGTCTCACATCCCTGA---

[illegible]

Consensus

gi|1255068|U50415
gi|163210|M77120
gi|165950|M96845
gi|1730275|U34273
gi|186334|M13982
gi|186336|M23442
gi|294220|L12991
gi|3005104|AF046213
gi|33831|X06750
gi|52678|X05064
gi|52678|X05064b
gi|52682|X05253
gi|533236|M25892
gi|790828|L37779

Figure 131

Figure 132

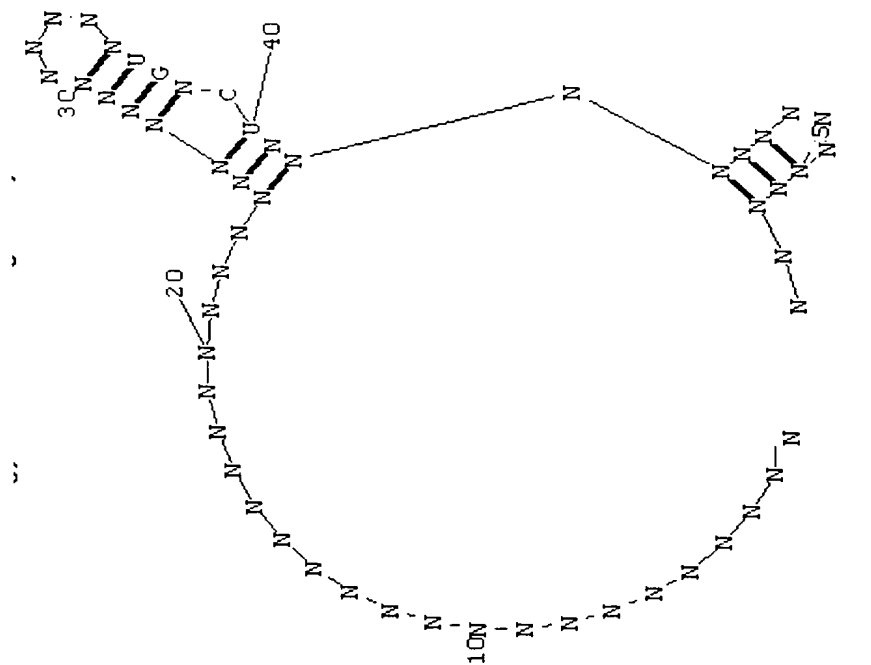


Figure 133

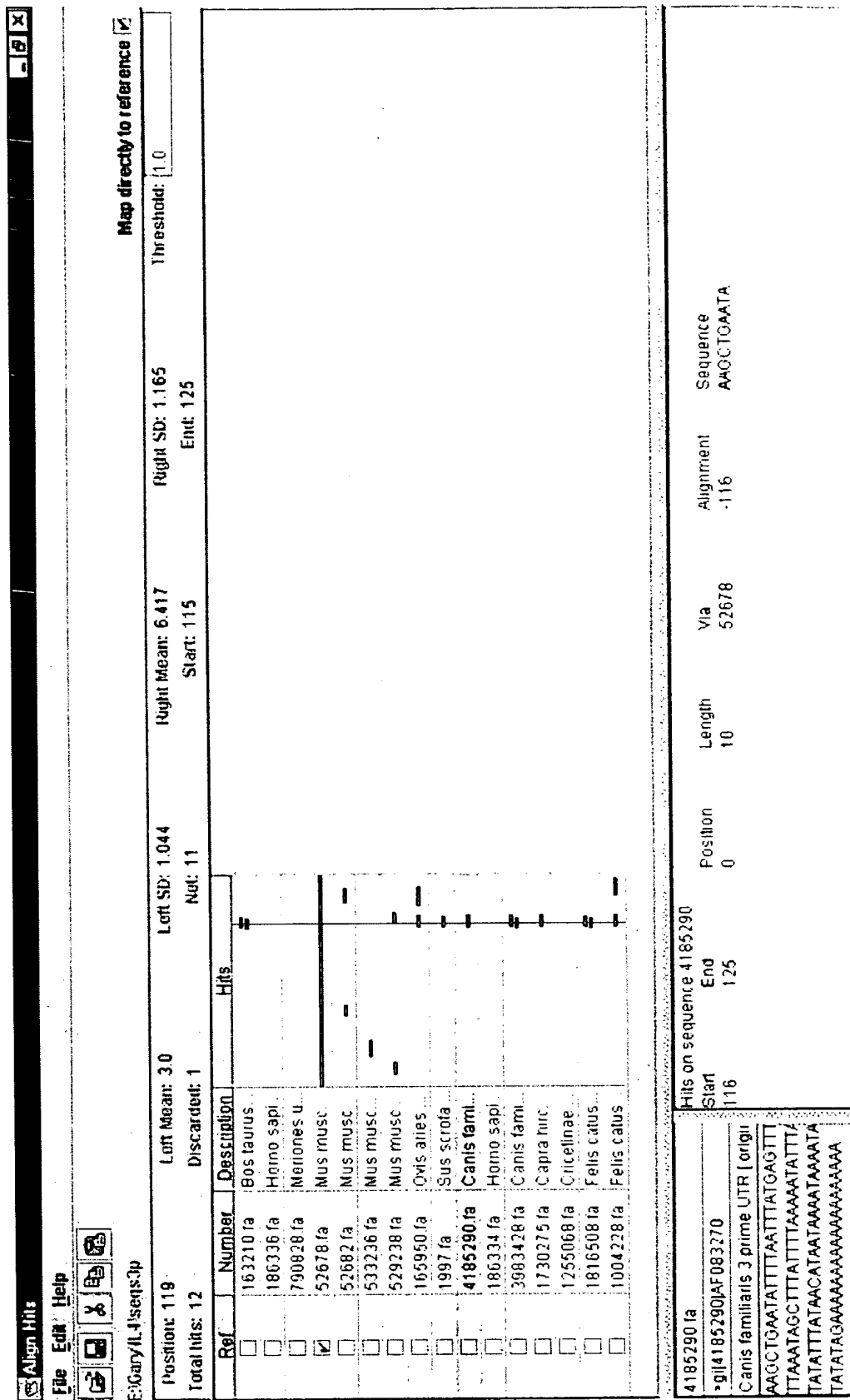


Figure 134

CLUSTAL W (1.74) multiple sequence alignment

```
gi|1004228|X87408      TTATAATTATTATATAAATAAGTATATATGT-
gi|1004228|X87408b    XXXXXAAGCTGAATATCTTAAATTTATGAG
gi|163210|W77120      ATGTAGAGCTGAAAAAAXXXXXXXX
gi|163210|W77120b     XXXXXAAGCTGAATATTTTAAATTTATGAG
gi|165950|W96845      AATTTATGCTTTTAAATAGCTTATAT---
gi|165950|W96845b    XXXXXAAGCTGAATATTTTAAATTTATGAC
gi|1730275|U34273     XXXXXAAGCTGAATATTTTAAATTTATGAC
gi|1816508|U39634     ATGTAGAACTGAAAAAATAAATAAATAA
gi|1816508|U39634b   XXXXXAAGCTGAATATCTTAAATTTATGAG
gi|1997|X68330        XXXXXAAGCTGACTATTTTAAATTTATGAT
gi|3983428|AF104245   ATATAGACCTAAAAAATAAATAAATAAAXX
gi|3983428|AF104245b XXXXXAAGCTGAATATTTTAAATTTATGAG
gi|4185290|AF083270  XXXXXAAGCTGAATATTTTAAATTTATGAG
gi|52678|X05064       ACACGAATCTGAATGAGAAATGCCCTGTGAT
gi|52682|X05253       ACTTCATTGCCATAAGGTTCTACTGTTAG
gi|529238|L32955      ATAAAAACAACAACTTCCTCCXXXXXXX
gi|529238|L32955b    GTGTCCCACTGAAGGAGCAAGGCTCAGGC
```


2000-2001 and 2001-2002
The data from the 2000-2001
and 2001-2002 seasons are
presented in the following
tables.

Figure 136

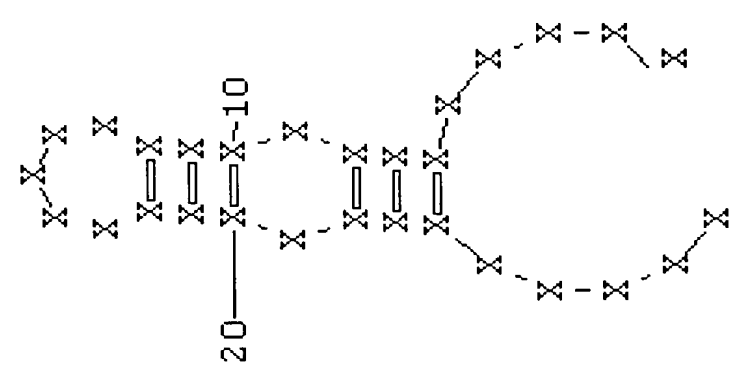


Figure 137

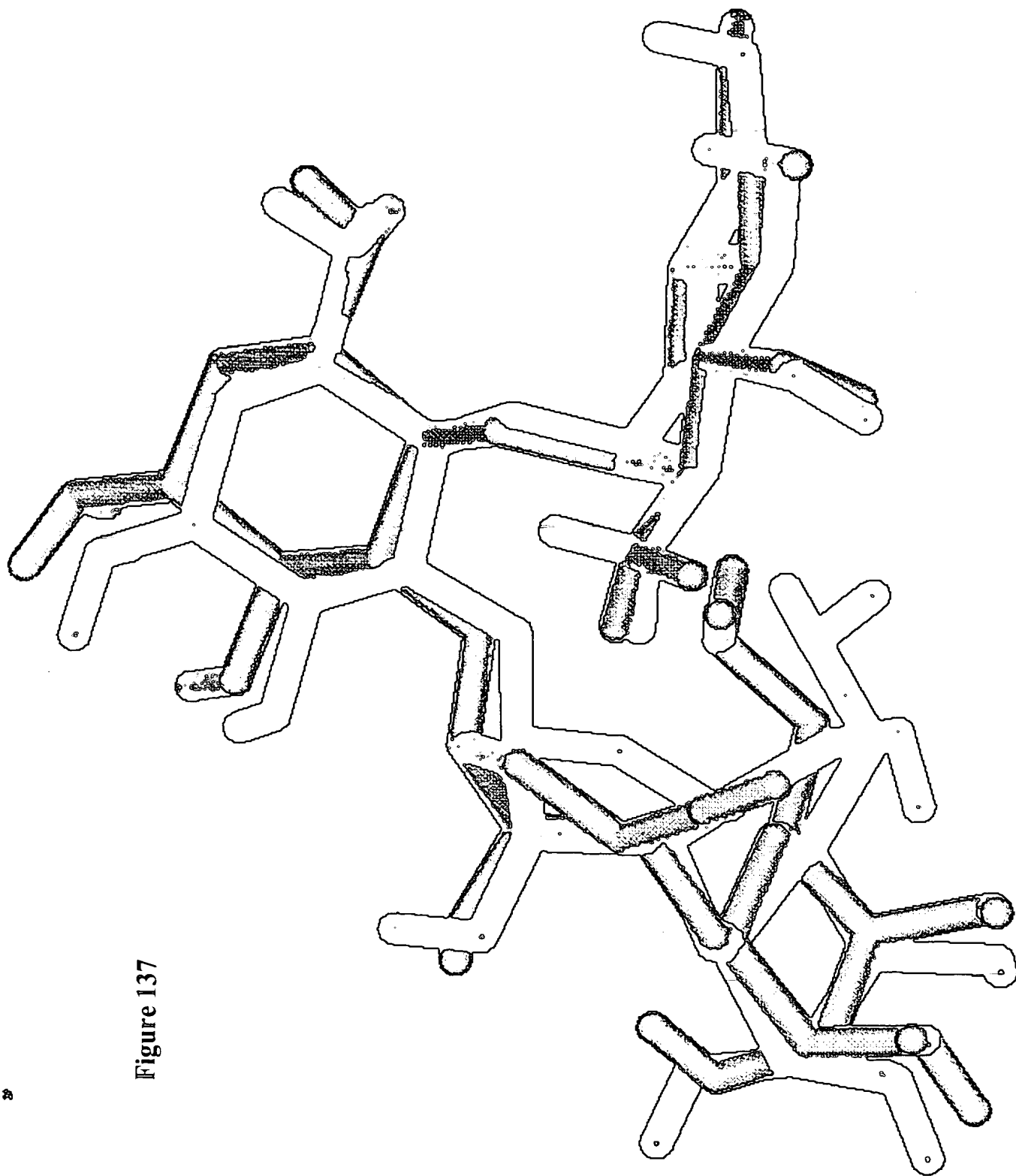


Figure 138 shows the energy score vs. RMSD for the 15 different models. The x-axis represents the RMSD (Root Mean Square Deviation) in Angstroms, ranging from 0 to 60. The y-axis represents the Energy score, ranging from 0 to 3. The legend indicates that the models are represented by different symbols: 12 (diamond), 11 (square), 13 (circle), 14 (cross), and 15 (asterisk).

Energy score vs. RMSD

Figure 138

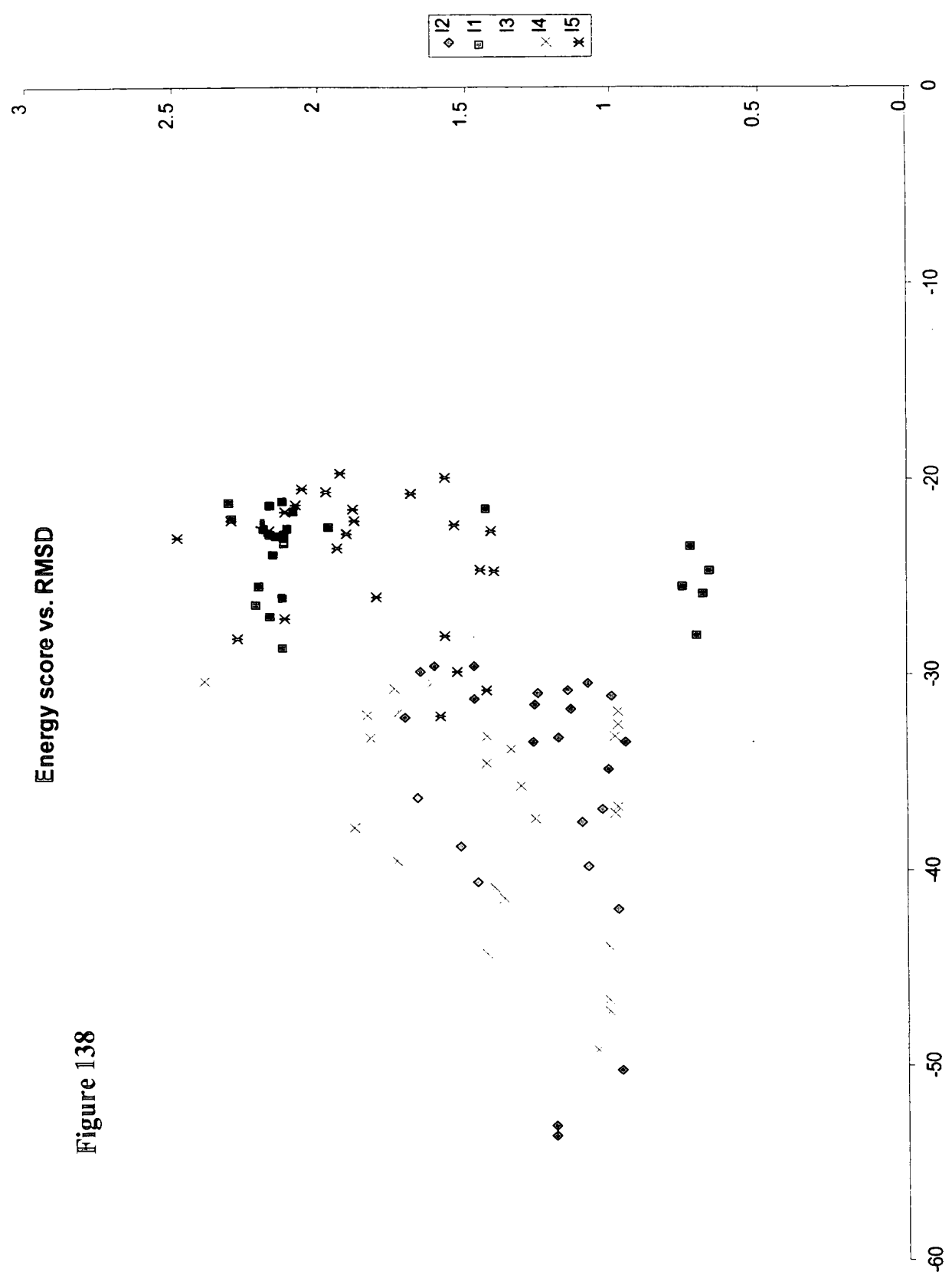


Figure 139

MASS of 60-Member Ibis Library Against 16S A-site RNA

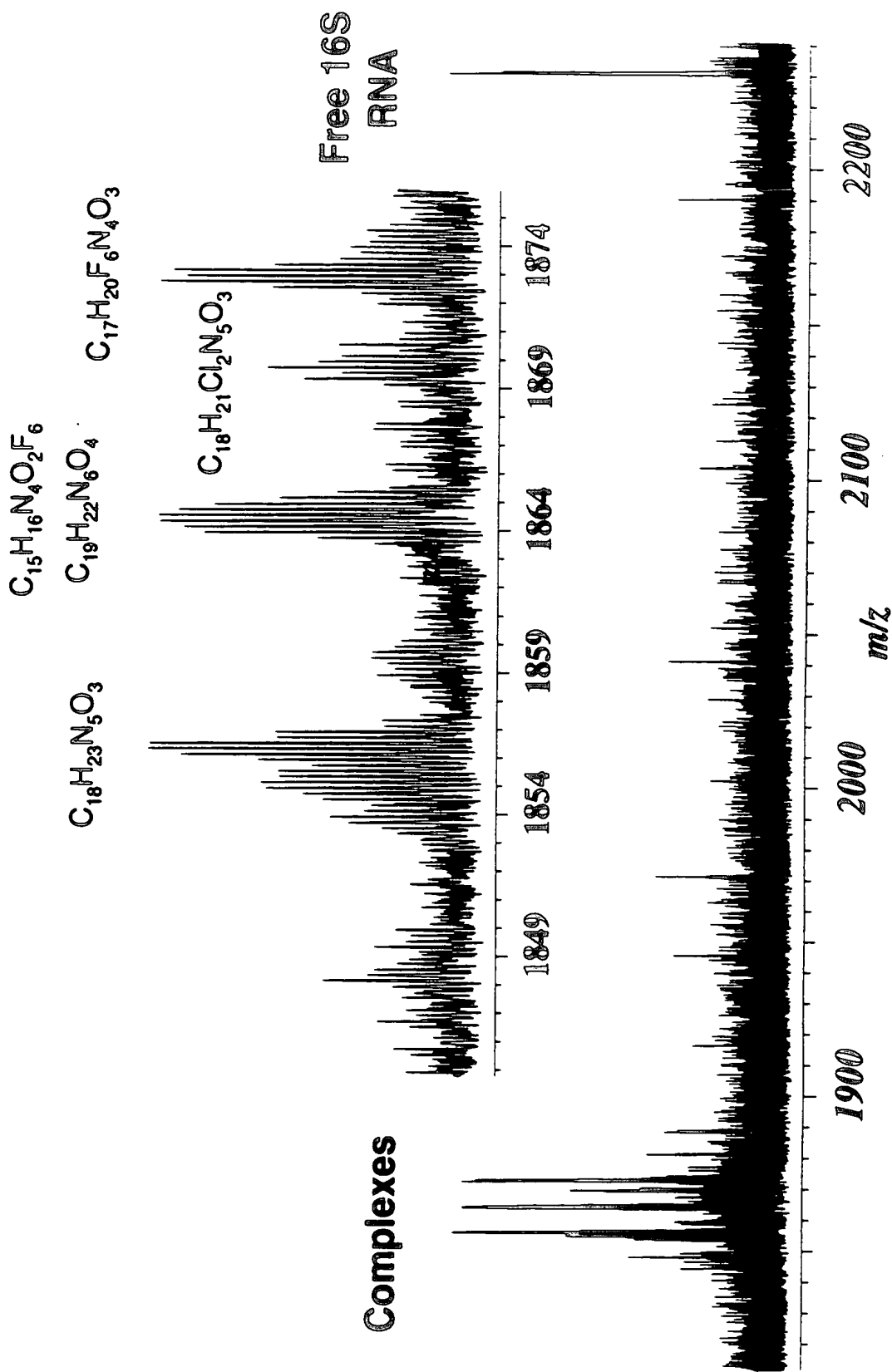


Figure 140

MASS of 60-member Library against 16S A-site Model

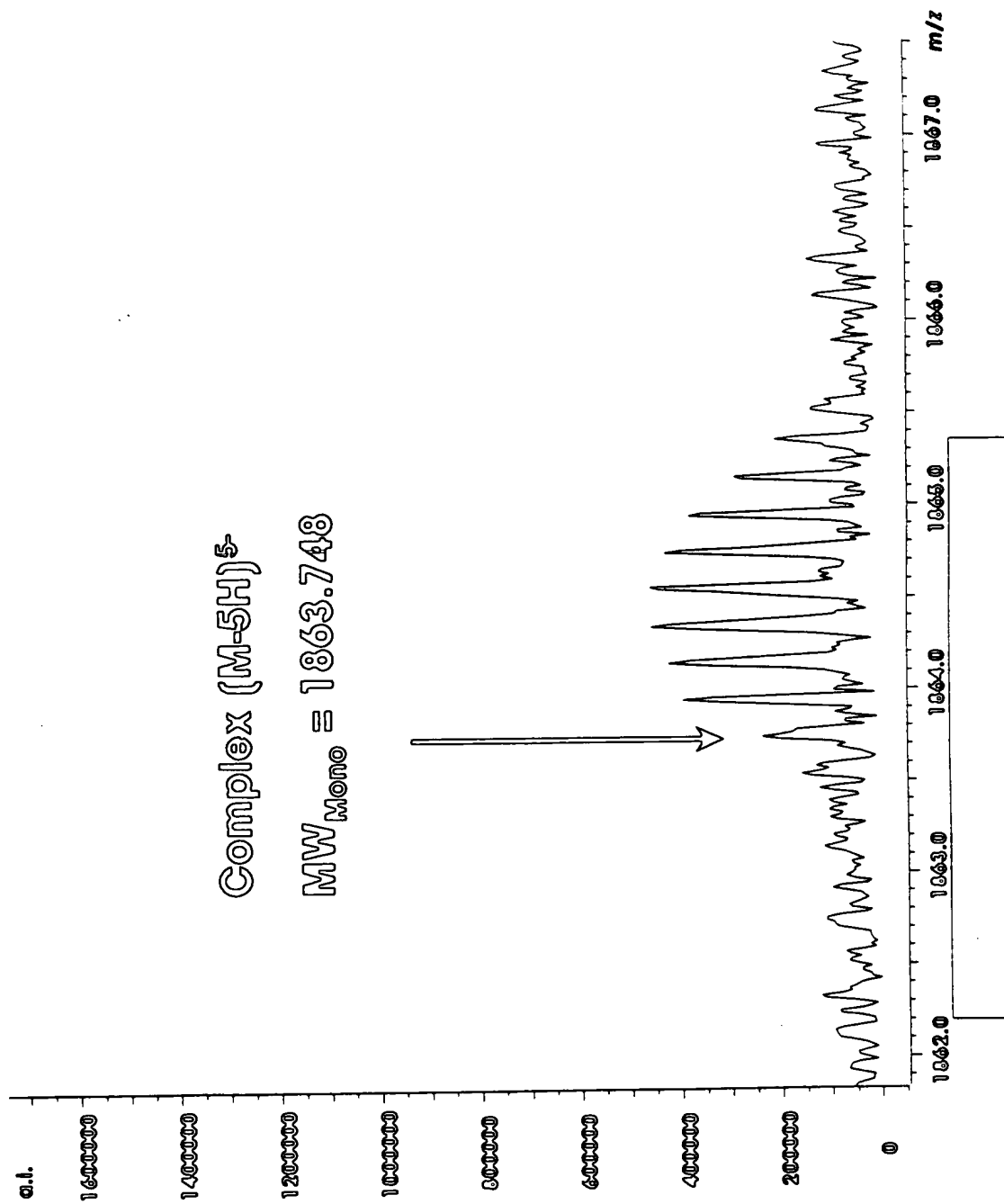


Figure 141

FT-ICR MS of Starting Library

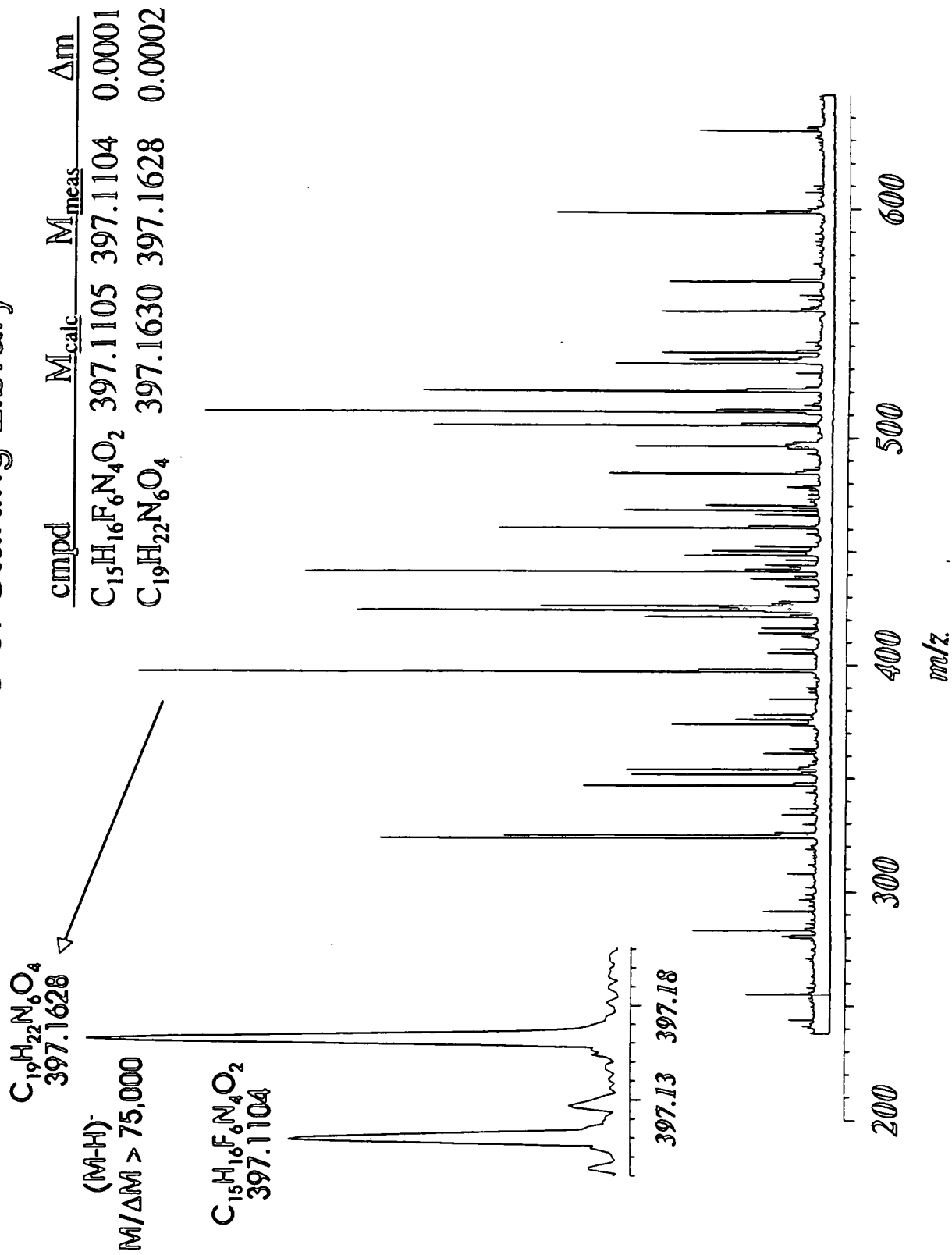


Figure 142

Compound Identification from a 60-member Combinatorial library with MASS

Complex M _{meas}	9320.300±.009 Da
RNA M _{meas}	8922.189±.009
ΔM	398.111±.009 Da

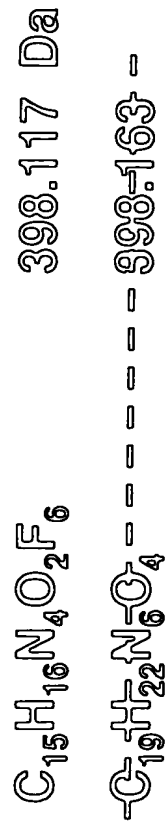


Figure 143

Elemental Composition Constraints

Measured Mass: 615.2969

Mass Tolerance: 1.0 ppm

Charge: 0

Element Min. atoms Max. atoms

¹² C	12	30
¹ H	23	60
¹⁶ O	7	20
¹⁴ N	3	20

Possible Elemental Compositions:

Calc. Mass Error Molecular Formula

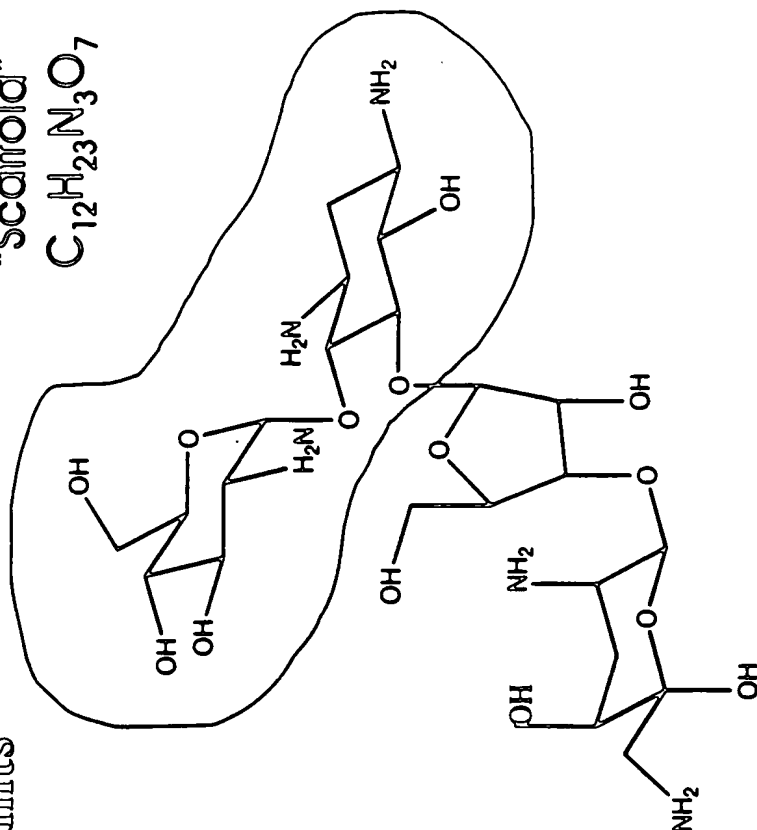
(amu) (ppm)

615.296291	0.98	¹⁶ O ₄ ¹⁴ N ₁₉ ¹² C ₂₁ ¹ H ₃₃
615.296298	0.98	¹⁶ O ₉ ¹⁴ N ₁₂ ¹² C ₂₂ ¹ H ₃₉
615.296305	0.97	¹⁶ O ₁₄ ¹⁴ N ₅ ¹² C ₂₃ ¹ H ₄₅
615.296808	0.15	¹⁶ O ₁₅ ¹⁴ N ₁₇ ¹² C ₈ ¹ H ₄₁
615.296815	0.14	¹⁶ O ₂₀ ¹⁴ N ₁₀ ¹² C ₉ ¹ H ₄₇

Further constrain by elemental composition of "letters"

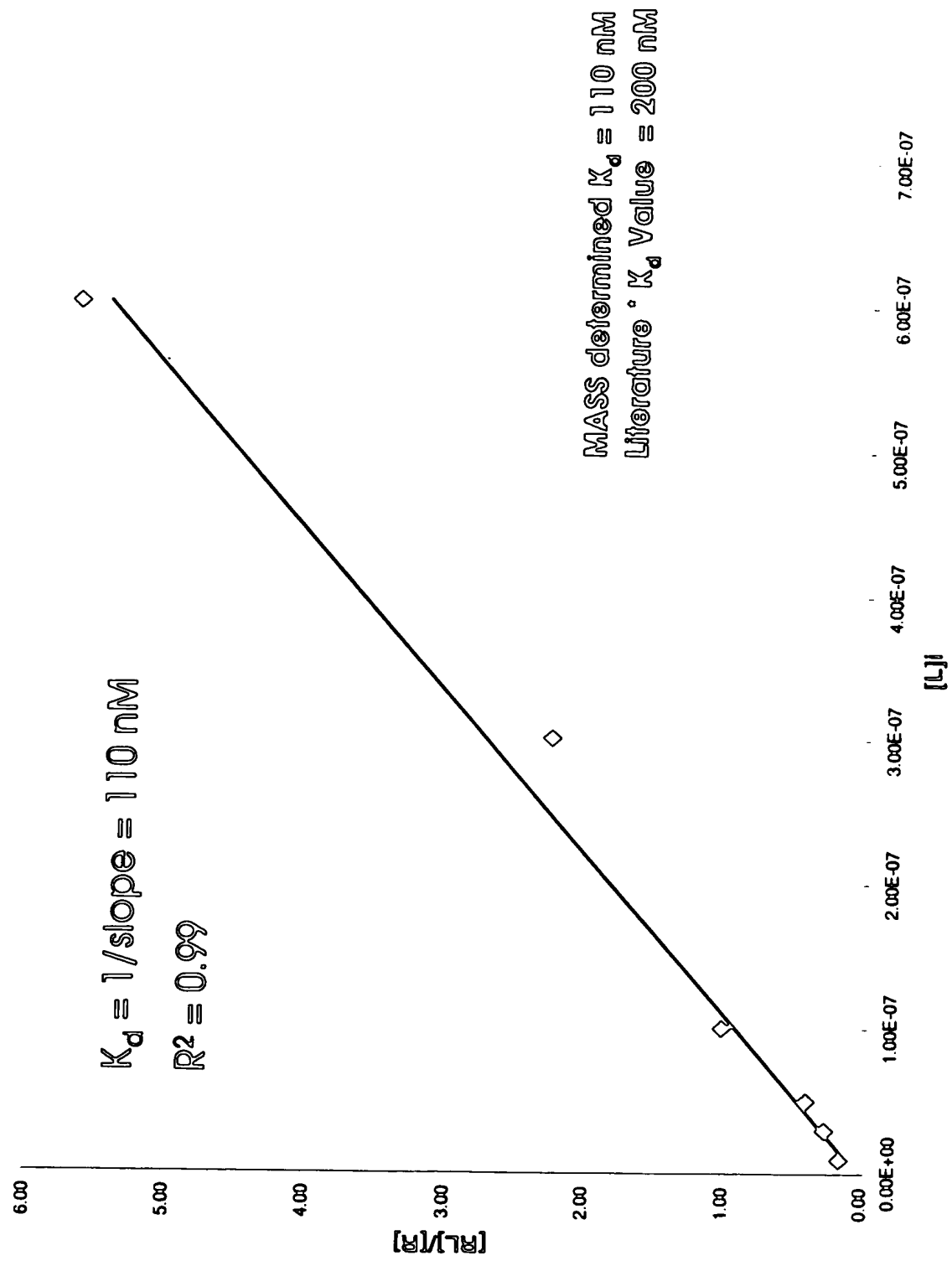
unintended products...

"Scaffold"
C₁₂H₂₃N₃O₇

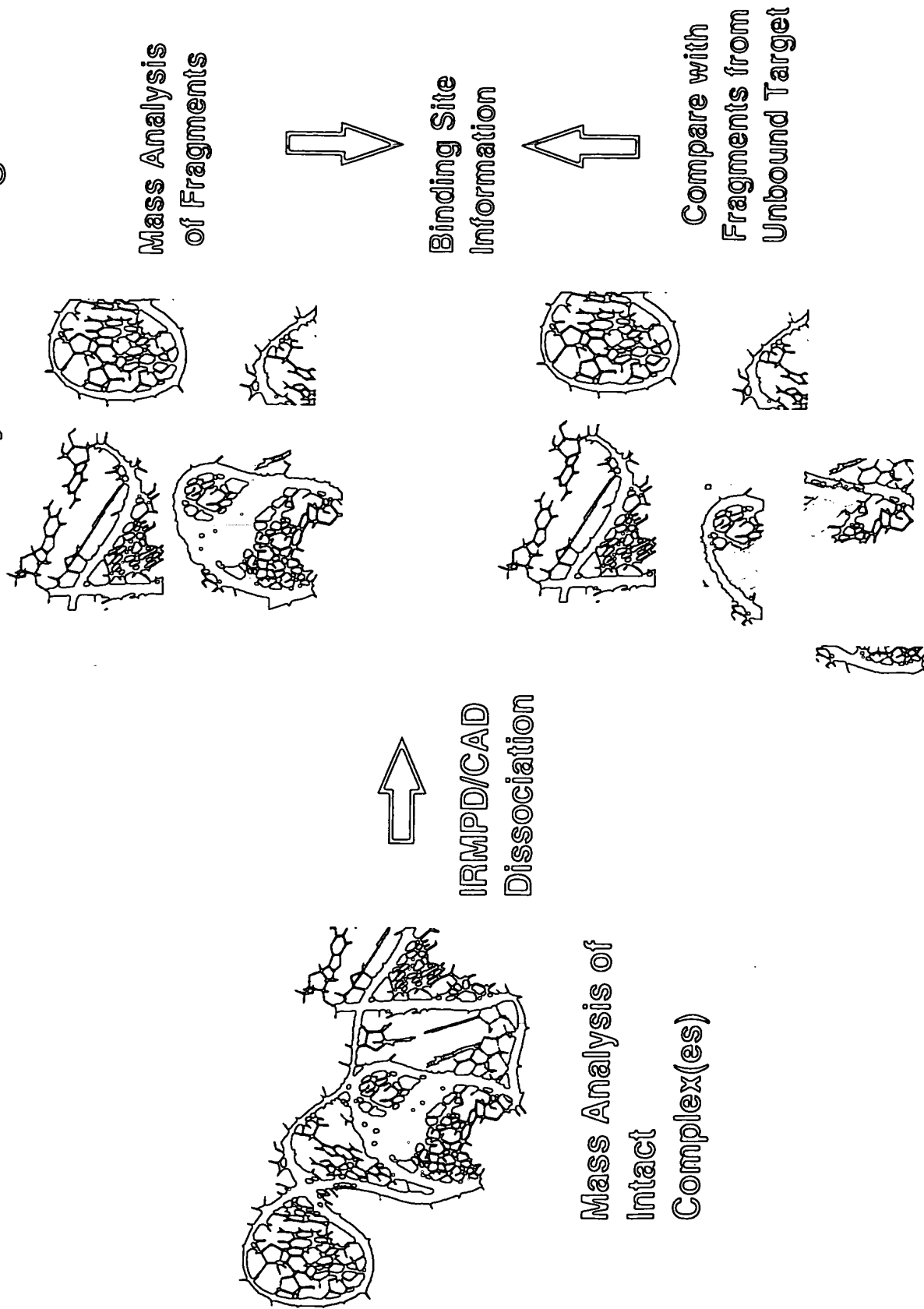


MASS K_d determination for 16S-Paromomycin

Figure 144



Multitarget Affinity/Specificity Screening



(16S+1bis564)5-

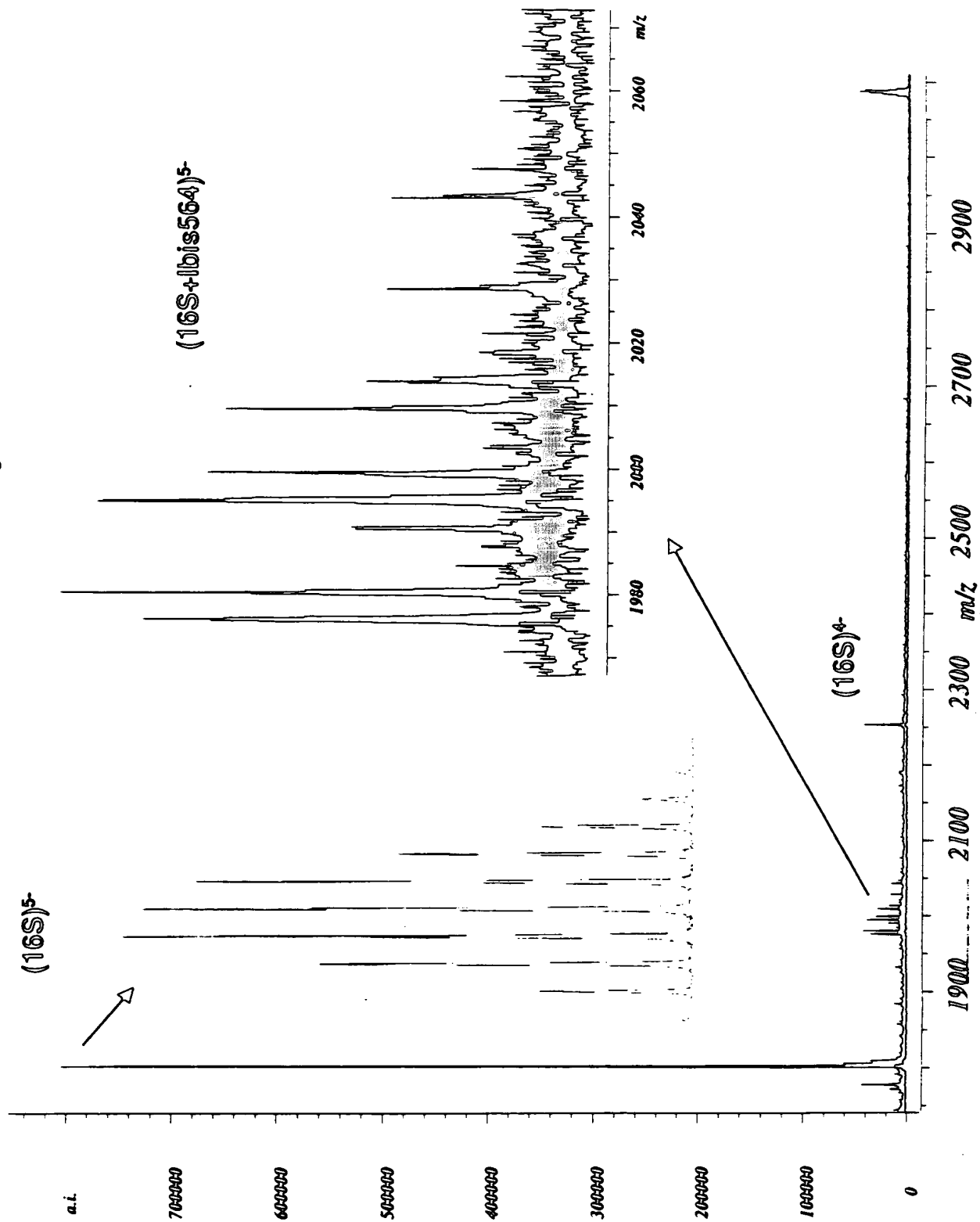


Figure 147

MASS Protection Assay

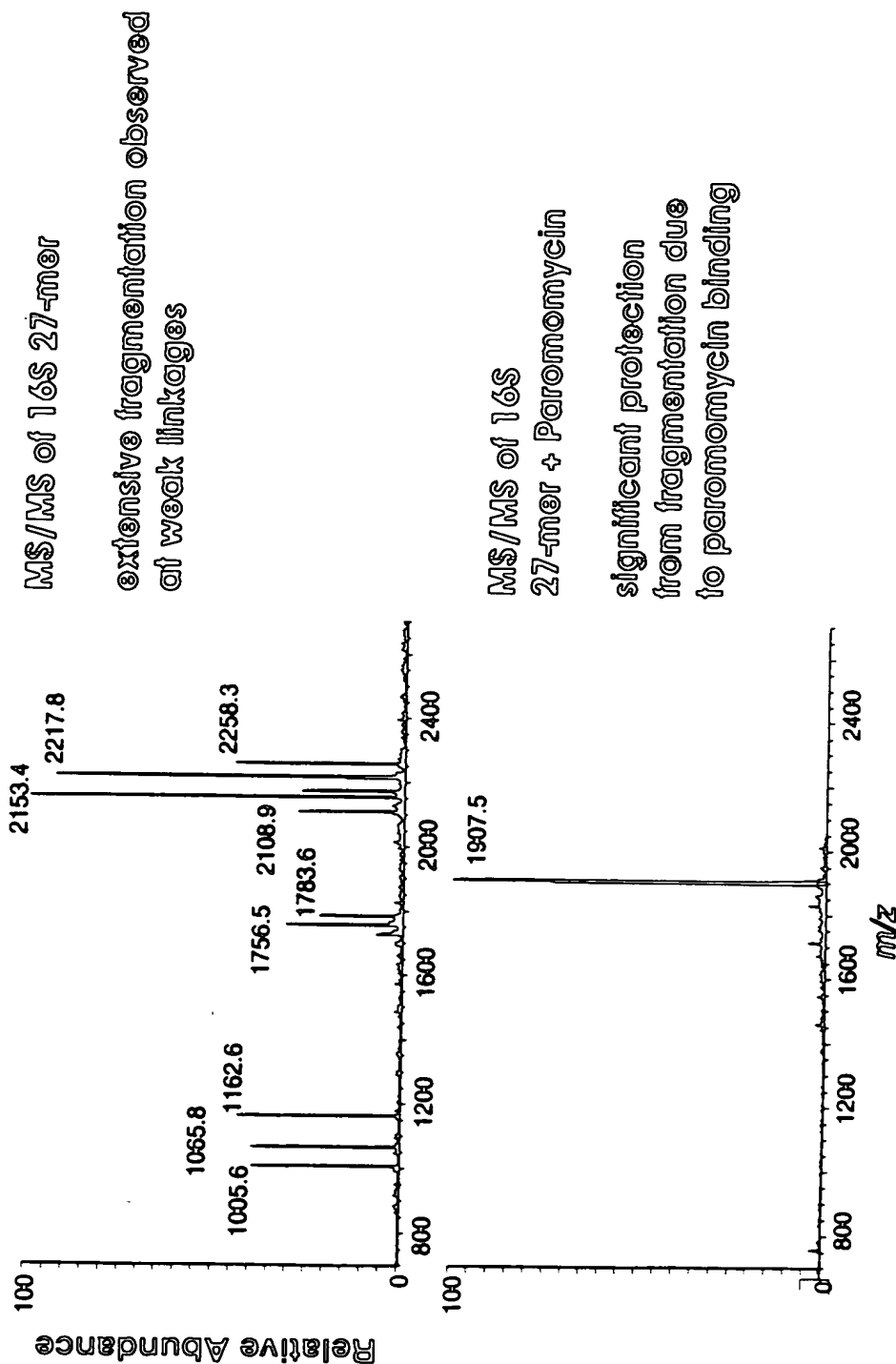


Figure 148

MASS Protection Assay

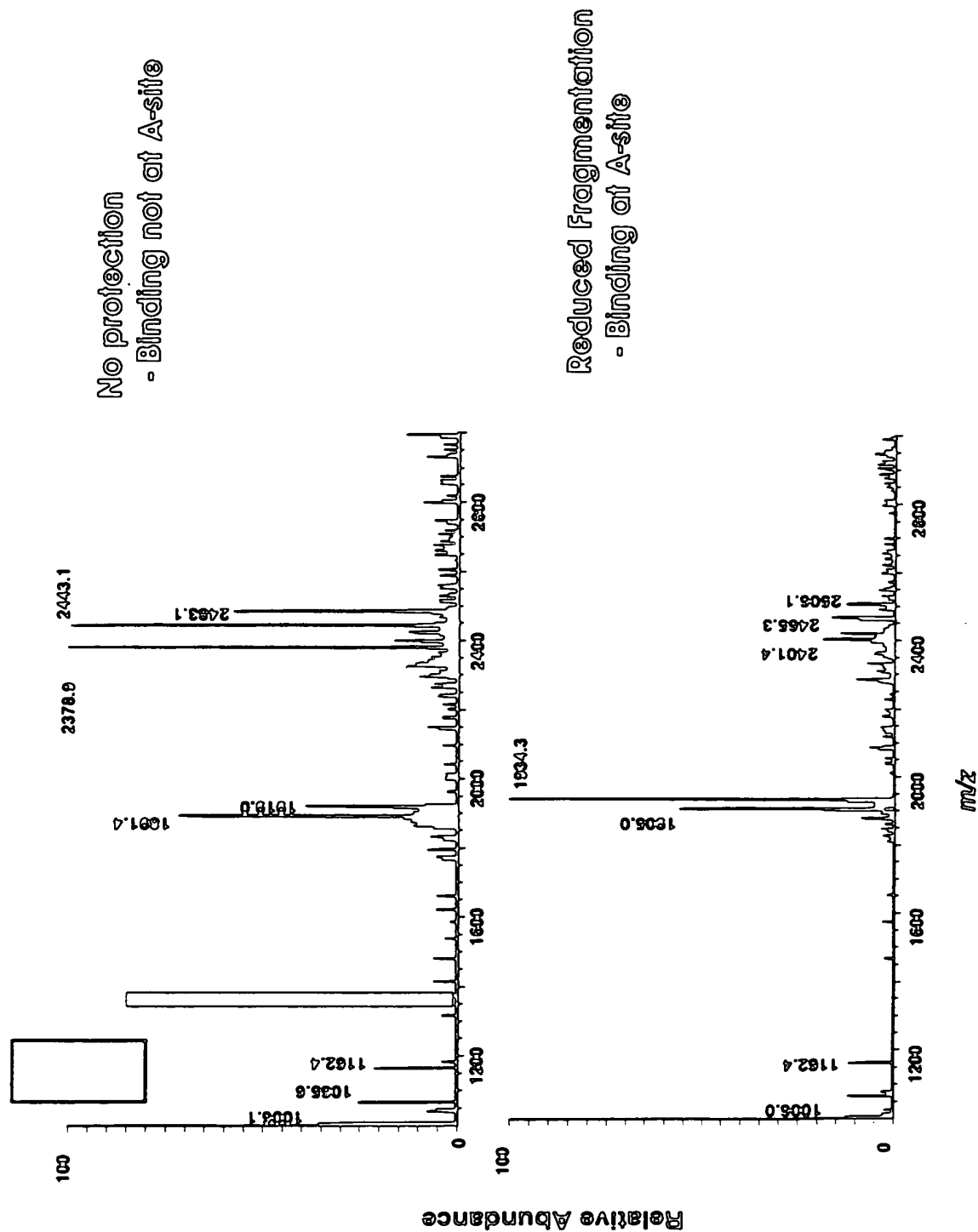
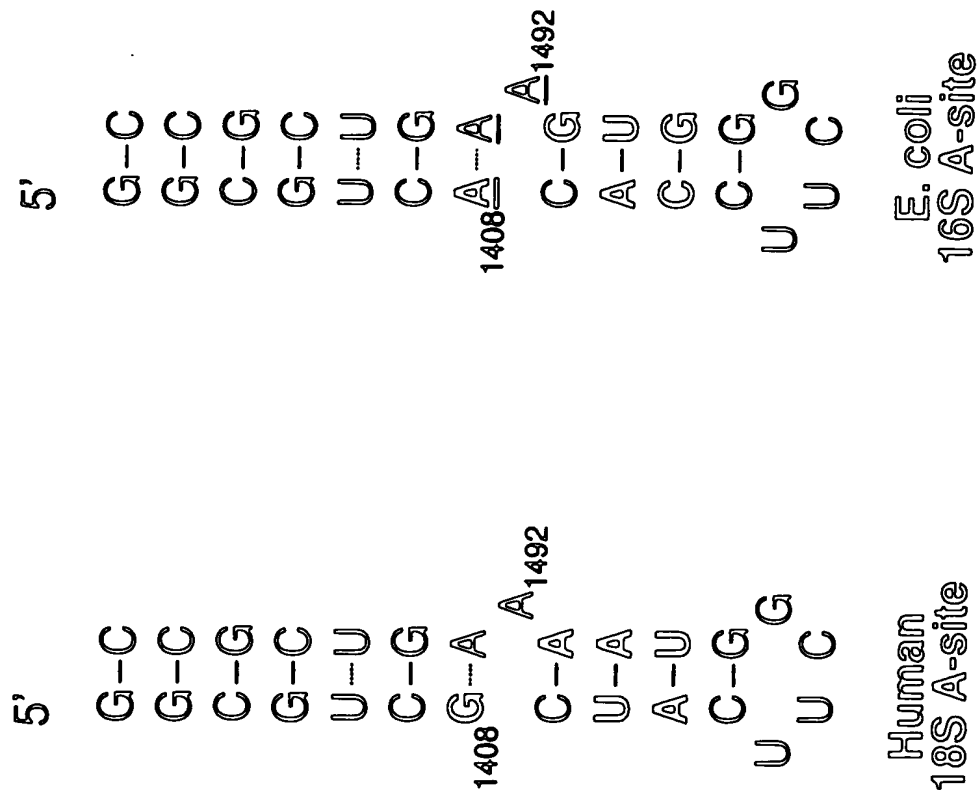


Figure 149

Eukaryotic and Prokaryotic A-Sites

Aminoglycoside antibiotics bind to

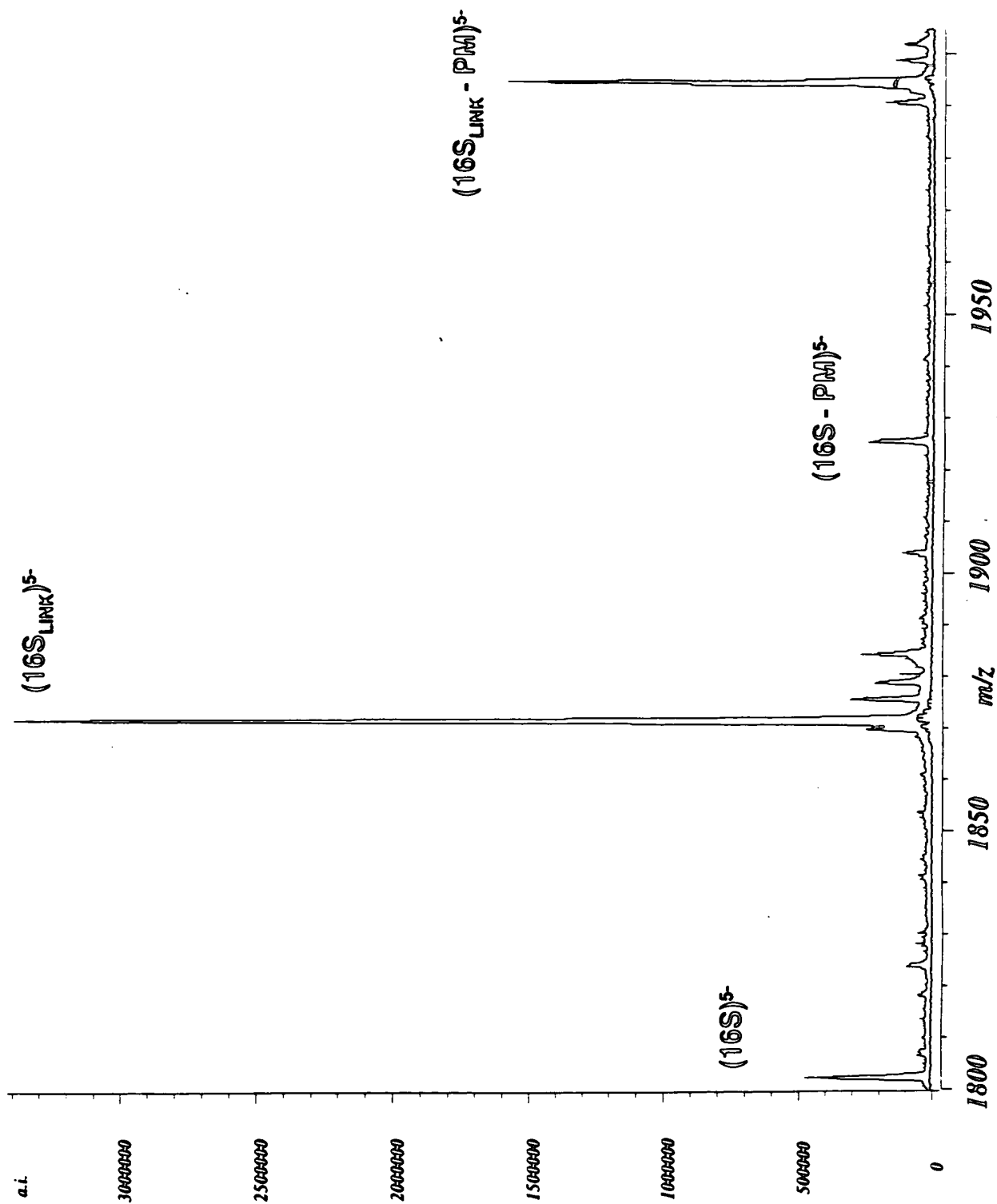
A-site of decoding region in 16S RNA



Δ MW = 15.011 Da

Neutral Mass Tag Does Not Affect Ligand Binding

Figure 150



Simultaneous Screening of 16S A-site and 18S A-site Model RNAs Against Aminoglycoside Mixture

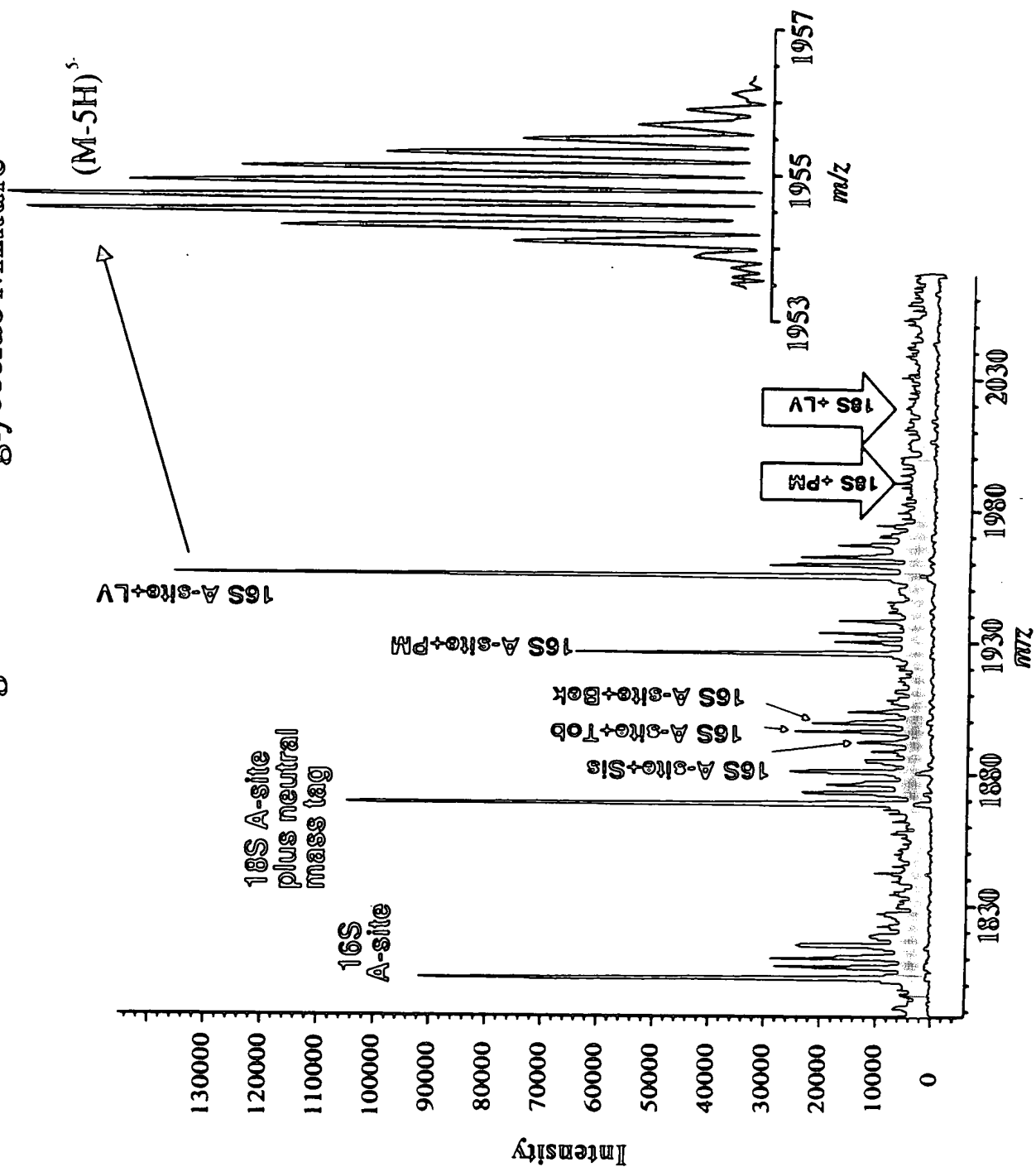


Figure 152

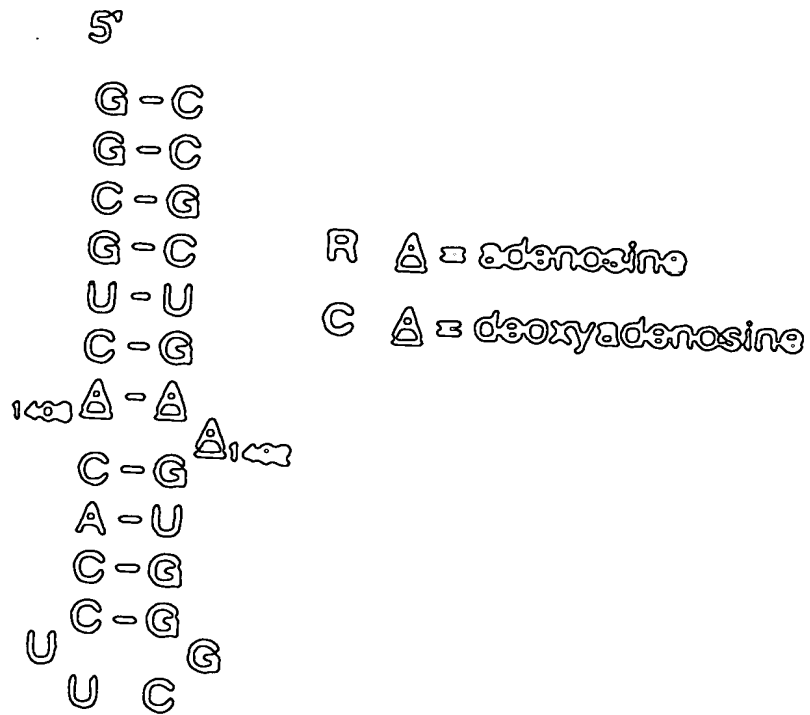


Figure 153

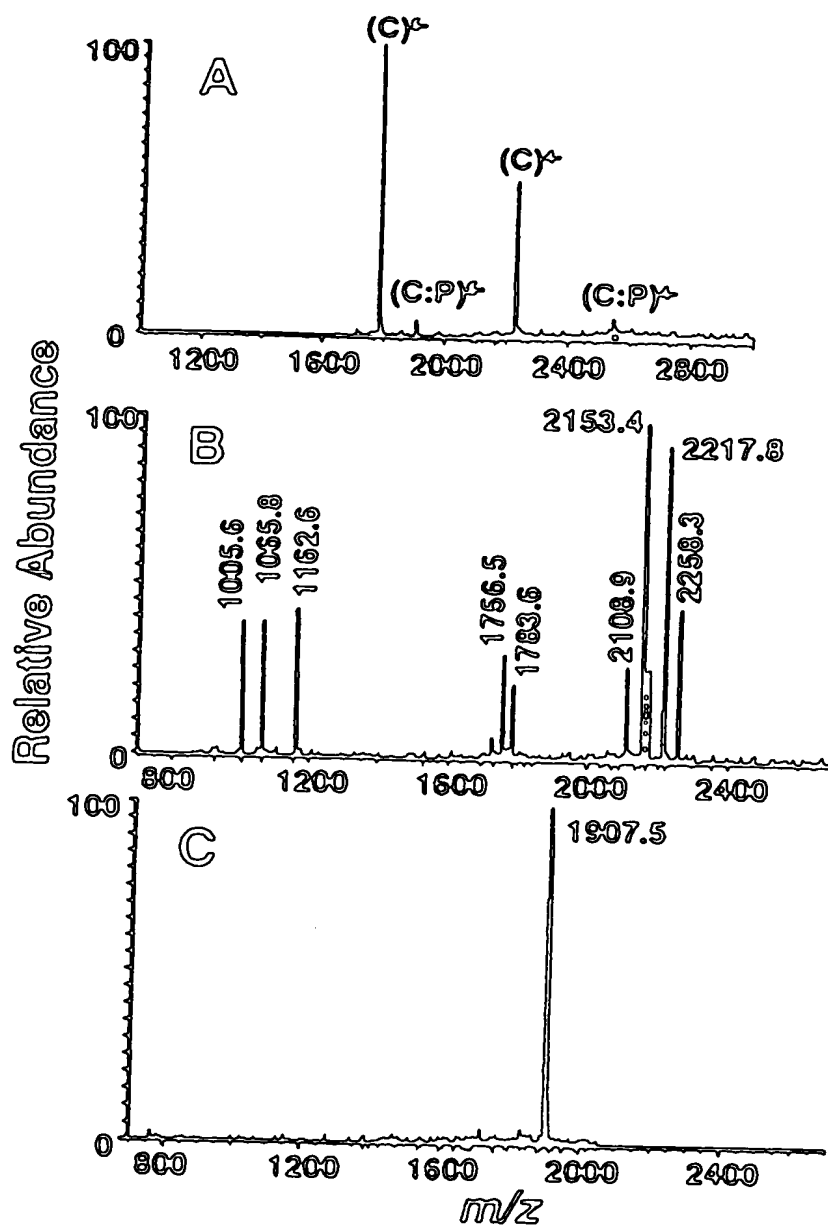


Figure 154

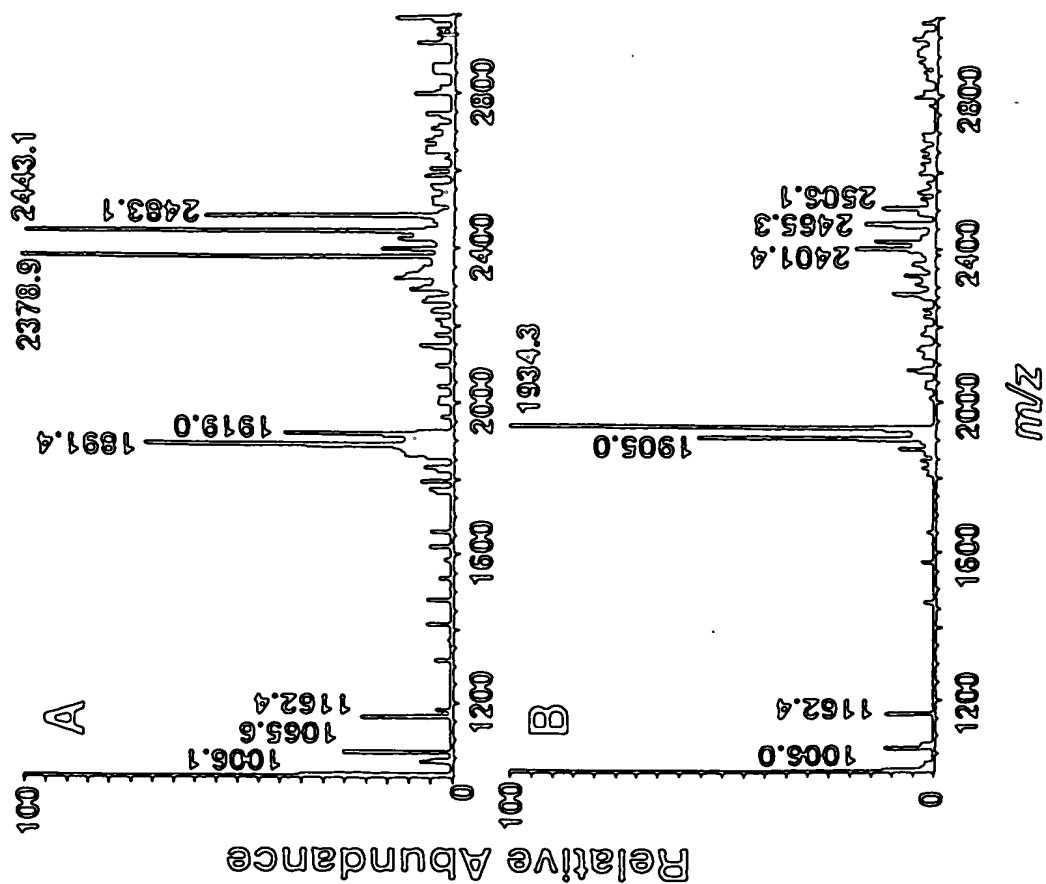


Figure 155

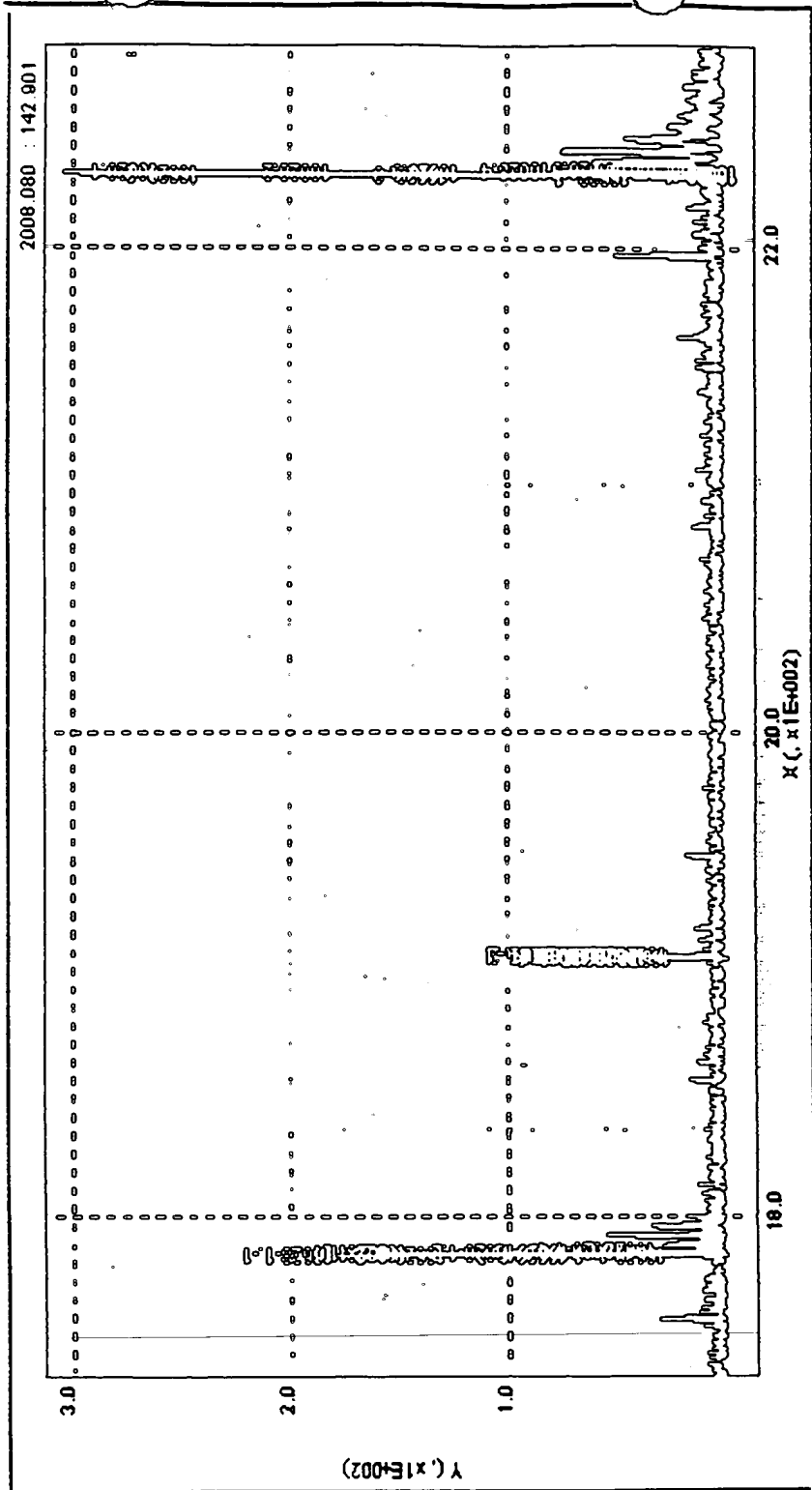


Figure 158

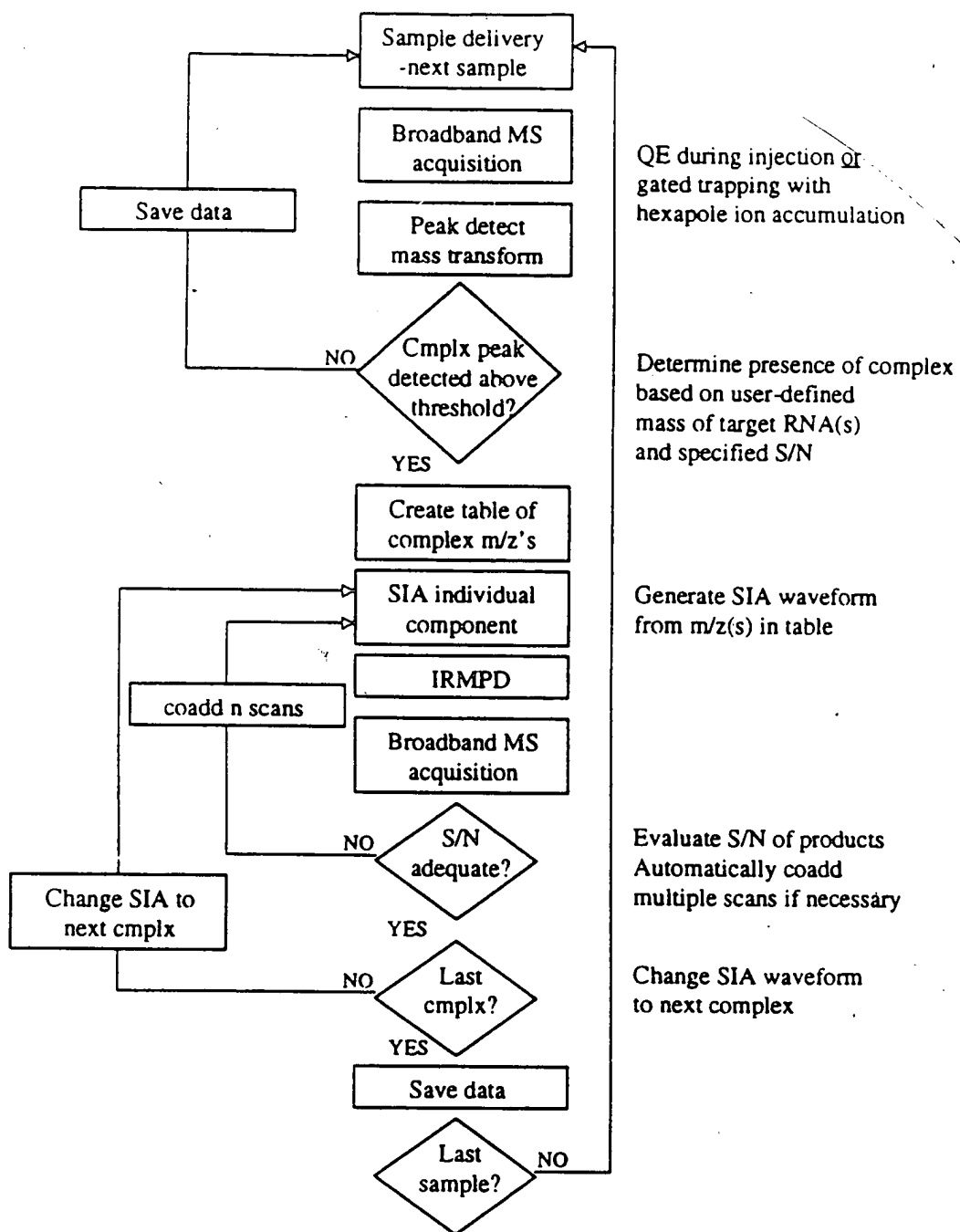


Figure 157

nr	name	apex	start	stop	height	area
1	16628-1-4	1783.710	1783.635	1783.834	14.55	1.63
2	16628-1-3	1783.909	1783.834	1783.972	60.04	5.15
3	16628-1-2	1784.109	1784.021	1784.184	115.60	11.14
4	16628-1-1	1784.308	1784.233	1784.383	167.34	15.89
5	16628-1.0	1784.508	1784.433	1784.620	133.94	14.74
6	16628-1.1	1784.707	1784.620	1784.795	136.60	13.38
7	16628-1.2	1784.907	1784.795	1784.982	82.63	8.56
8	16628-1.3	1785.107	1785.032	1785.219	57.81	5.21
9	16628-1.4	1785.306	1785.232	1785.369	32.31	2.65
10	16628-1.5	1785.506	1785.456	1785.569	17.67	1.12
11	16628.10019-4	1906.974	1906.874	1907.031	12.63	1.00
12	16628.10019-3	1907.173	1907.045	1907.273	22.54	2.11
13	16628.10019-2	1907.373	1907.287	1907.444	33.86	2.91
14	16628.10019-1	1907.572	1907.458	1907.701	34.87	3.30
15	16628.10019.0	1907.772	1907.701	1907.843	20.93	1.55
16	16628.10019.1	1907.972	1907.900	1908.043	21.03	1.55
17	16628.10019.2	1908.157	1908.086	1908.271	10.97	0.90
18	16628-4	2229.874	2229.679	2230.029	27.51	4.87
19	16628-3	2230.146	2230.029	2230.263	111.72	16.23
20	16628-2	2230.380	2230.263	2230.516	225.18	32.39
21	16628-1	2230.633	2230.516	2230.770	280.66	40.90
22	16628.0	2230.887	2230.770	2231.023	287.24	41.95
23	16628.1	2231.140	2231.023	2231.257	242.23	34.17

Graph Table